

# **FIGURE 1**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATG  
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGT  
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTT  
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG  
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTTTTATGCATTG  
CTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAAA  
TTAAACAAGGCTGGCCTTGACTTGAATACTGAGTTGTTTAGGACTTTCTATTGTGGCAAACCTT  
CCAGAAAACAACCCCTTTTTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCAT  
TATATATGTTTGTTCAGACCATCCTTTCTACCAAATGCAGCCCAAATCCATGGCAAACAAGTC  
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTAGCATGCTGACTTGCTC  
ATCAGTTTTGCACAGTGGCAATTTTGGGACTGATTAGAACAGAACTCCATTGGAACCCCGAGG  
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTT  
GGTTTTTTCCTGACTTACATTTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA  
TGGATTAACCCCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA  
GAGATATTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG  
TTCACAGAAGTTGCTTATTCTTCTCTGAAATTTCAACCACTTAATCAAGGCTGACAGTAACACT  
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCAT  
CAAGAAGACTATTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACT  
ATG

## **FIGURE 2**

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV  
LCIATIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG  
MGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW  
NPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR  
LLSRDI

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 13-33

#### **Other Transmembrane domains:**

amino acids 54-73, 94-113, 160-180, 122-141

#### **N-myristoylation sites.**

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

### FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACC  
GTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTC  
CTTACACTTCGCCATGAGTTTCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTG  
GATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTAGTATGTTGTACAG  
GTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATCTTTGAAATCTTAGG  
AGTATTGAATAGCAGCTCCCGTTATTTTCTGGAATAATGAACCTGTGTGAATTCTGCTGATCCTGG  
TTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAAACAACGA  
CTGCTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGAAACTAGGAGATCCCTTTCC  
CATTCTCAGCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTGGTGTGATTGGAG  
TGACTCTCATGGCTCTTCTTTCTGGATTTGGTGCTGTCAACTGCCCATACACTTACATGTCTTACTTC  
CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT  
CATAAGCAAAAAGAAAAGGATGGCAATGGCAGCGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACA  
AACCATCAGGTTTCTGGGGAATGATAAAAGTGTACCCTTCAGCATCAGGAAGTGAAATCTTACT  
CTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTCTGGAACAGCTGATCT  
ATATGCTACCAAGGAGAGAATAGAATACTCCAAACCTTCAAGGGGAAATATTTAATTTCTTGGTT  
ACTTTTTCTCTATTTACTGTGTTTGGAATTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTT  
GGGAAACCGGATCCTGTCAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT  
GAAGTTTGGTCCCAACACATTTCTTCATTCTTGTGGAATAATCATCGTCACATCCATCAGAGGAT  
TGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCAATGTCTG  
CTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTT  
AGAATACCGCACCATAATCACTGAAGTCCTTGGAAGTGCAGTTCAACTTCTATCACCGTTGGTTTG  
ATGTGATCTTCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACCA  
GAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAATTTA  
GATATAAGAGGGGGGAAAAATGGAACCGGGCCTGACATTTTATAAACAAACAAAATGCTATGGTAGC  
ATTTTTACCTTCATAGCATACTCCTTCCCCGTGAGGTGATACTATGACCATGAGTAGCATCAGCCAG  
AACATGAGAGGGGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG  
TGTAGAGCGGAGAGGAGCCAAGAACTAAAGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGT  
CTATGGTAGCTGAGCCAAACAGTAGGATTTCCGTTTTAAGGTTACATGGAAGGTTATAGCTTTG  
CCTTGAGATTGACTCATTAAATCAGAGACTGTAAACAAAAAAAAAAAAAAAAAAGGGCGGCCGCG  
ACTCTAGAGTCGACCTGCAGAAGCTTGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATG

## **FIGURE 4**

MSFLIDSSIMITSQILFFGFGWLFEMRQLFKDYEIRQYVVQVIFSVTFASFCTMFELIIFEILGV  
 LNSSSRYPFHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFFWKLGBP  
 FPILSPKHGILSIEQLISRVGVIGVITLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERRLLQ  
 TMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTTLIQEVDALAEELSRQ  
 LLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVGKTDVPVTRGIEI  
 TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLLAQIMGY  
 FVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

**Important features:**

**Signal peptide:**

amino acids 1-23

**Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
 425-444

**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

**Eukaryotic cobalamin-binding proteins**

amino acids 151-160



## FIGURE 5

AGCAGGGAAATCCGGATGTCTCGGTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC  
 AGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGT  
 GTTTCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT  
 TCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGT  
 GTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGCCAACCAGCAGCTGAATTTACAG  
 AAGCTAAGGAGGCCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCC  
 TTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGGATGGATTCTGGTCTATCTCTAG  
 GATTAGCCCAACCCCAAGTGTGGGAAAAATGGGTGGGTGTCTGATTGGAAGGTTCCAGTGA  
 GCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATTCCAGAA  
 ATTATCACCACCAAGATCCCATATTCAACACTCAAAGTGAACACAAACAAGAAATTTATTGT  
 CAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCCCTACTACTCCTC  
 CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGTGTGCAGAAAGTTTTATG  
 GAACTAGCACCATGTCTACAGAACTGAACCATTGTTGAAAATAAAGCAGCATTCAAGAATGA  
 AGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTGCTCTCCTCTCTTTGGTGCTG  
 CAGCTGGTCTTGGATTTTGCTATGTCAAAGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAT  
 CAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCATA  
 TGAGGAATCAAAGAAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGC  
 GATGCCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTTCTT  
 CATGCTCCTTACCCTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAGAAGAAAGTCCA  
 CCCTTGCTTCCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAT  
 GCCCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTAGCTCCAAAGCTTCCCACGGCCT  
 TTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGAAGGAC  
 CTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGGTG  
 AAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGACCTTTCTTCA  
 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTGAGCCCGGTAAGAGCAAAAGAAT  
 GGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAA  
 GCTAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTGAGCAGGGACTGTAAAC  
 ACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACA  
 CTTACTTTTTCTGGTCTCTACCACTGTCTGATATTTCTCTAGGAAATATACTTTTACAAGTAACA  
 AAAATAAAAACCTTTATAAATTTCTATTTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATT  
 ACTCAGTAATTTGTTTAAAAAGTAATAAAATTCAACAAACATTTGCTGAATAGCTACTATATGTC  
 AAGTGCTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCCTCAAAAAATTGCACATAGTAG  
 AACGCTATCTGGGAAGCTATTTTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAAACTAAT  
 TTTTATTTTTGCTGAGACTAATCTTATTCATTTTCTCTAATATGGCAACCATTTATAACCTTAATT  
 TATTATTAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAAGCACATTTTAAAAGTGCC  
 ATTAACAAATGTATCACTAGCCCTCTTTTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATT  
 TGTGACAAAAAATTAAAGCATTTAGAAAACCT

## **FIGURE 6**

MARCFSLVLLLSIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTAEKEACRLLG  
 LSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLWKVPVSRQFAAYCYN  
 SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPR  
 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGGVPTALLVLALLFFGAAAGLGFCYVK  
 RYVKAFPFNTKNQKEMIETKVVKEEKANDSNPNESKKTDKNPESKSPSKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 7

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCGAGCCCGGC  
GGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCCGGGCGG  
CGGCTGCGGGCGCAGAGCGGAGATGAGCGGCTTGGGGCCACCTGCTGTGCCGTGCTGCTGGCGG  
CGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGCCCGGCCG  
GCTCTCAGCTACCCGAGGAGGAGGCCACCTCAATGAGATGTTCCGCGAGGTTGAGGAACATGAT  
GGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTA  
AAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCAGCTATCACAATGAGACCAACACAGAC  
ACGAAGGTTGGAATAATACCATCCATGTGCACCGAGAAATTCACAAGATAACCAACAACAGAC  
TGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAAGAAGGCAGAAGGAGCC  
ACGAGTGCATCATCGACGAGGACTGTGGGCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTAC  
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAGTGTGTGGAGACCA  
GCTGTGTGTCTGGGGTCACTGCACCAAAATGGCCACCAGGGGCGCAATGGGACCATCTGTGACA  
ACCAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCCAGAGAGGCTGCTGTTCCTGTGTGC  
ACACCCCTGCCCGTGGAGGGCGAGCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCAC  
CTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGC  
CCCACAGCCACAGCCTGGTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGG  
GAGATCCTGCTGCCAGAGAGGTCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCG  
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTG  
CCGCCGCTGCACTGTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAA  
TAGAAATAGCTAATTTATTTCCCGAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTA  
CATCTTCTTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCAATTTGTTACAGCT  
CCCCCAGGCTGTTCTCCAGGCTTACAGTCTGGTGTCTGGGAGAGTCAGGACAGGTTAACTGCA  
GGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCCTTACCAGTTGGCAGACAGCCG  
TTTGTCTTACATGGCTTTGATAATTGTTGAGGGGAGGAGATGGAACAATGTGGAGTCTCCCTC  
TGATTGGTTTTGGGGAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAACCTGGCAAAAATG  
CAACAAATGAATTTTCCACGAGTTCTTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGC  
AGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTATTATCCAGCAGTGTGTGCTCAGCTCC  
TACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTCCTCTCTCAGCACAGCCTGGGG  
AGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCC  
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCT  
CTCCACTACCCACACACAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAAGGAGAATGGGAT  
TTTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAATAATTCTCACATCCCTCTAAAAGTAAA  
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGGCAGCCGCTTCTAATGAAGACAATGAT  
ATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCA  
TACAGGTTAACCTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGC  
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAAATCAACCGAGCAGGGC  
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATG  
TTTTCAGGTGTCATGGACTGTTGCCACCATGTATTATCCAGAGTTCTTAAAGTTTAAAGTTGCA  
CATGATTGTATAAGCATGCTTTCTTTGAGTTTTAAATTATGTATAAACATAAGTTGCATTTAGAA  
ATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 8**

MQRLGATLLCLLLAAVPTAPAPAPTATSAPVKPGPALSYQEEATLNEMFREVEELMEDTQHKL  
 RSAVEEMEAEAAKASSEVNLANLP SYHNETNTDTKVGNN TIHVHREIHKITNNQTGQMV FSE  
 TVITSVGDEEGRRSHECI IDEDCGPSMYCQFASFQYTCQPCRGQRM LCTRDSECCGDQLCVWGHC  
 TKMATRGSNGTICDNQRDCQPG LCCAFQ RGLLPVCTPLPVEGELCHDPASRLDLITWELEPDG  
 ALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQGEILLPREVPDEYEVGSFMEEVRQELEDLE  
 RSLTEEMALGEPAAAAAALLGGEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## FIGURE 9

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCAC  
GGCCACCTTGTGAACCTCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCATCCAAAG  
GCCTAATCCAACGTTCTGTCTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTCTGGACCTT  
AACTGGGTACTGGCCCTGGGCCAATGCGTCCCTCGCTGGAGCCTTTGCCTCCTTCTACTGGGCCTT  
CCACAAGCCCCAGGACATCCCTACCTTCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACC  
ACACTGGGTCAATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAGATAGCCCGGGTCATCTTG  
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGCCCGCTGCATCATGTGCTGTTT  
CAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCCTAACCGCAATGCATACATCATGA  
TCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTCATGCTACTCATGCGAAAC  
ATTGTCAGGGTGGTCTCCTGGACAAAAGTACAGACCTGCTGCTGTTCTTTGGGAAGCTGCTGGT  
GGTCGGAGGCGTGGGGGTCTGTCTTCTTTTTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAG  
ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCCATCATGACCTCCATCCTGGGGGCCTAT  
GTCATCGCCAGCGGCTTCTTCAGCGTTTTTCGGCATGTGTGTGGACACGCTCTTCCTCTGCTTCCT  
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAA  
AGATTCTGGGCAAGAAGAACGAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGAAGAGCTCCGG  
CCCTGATCCAGGACTGCACCCACCCACCCTCCAGCCATCCAACCTCACTTCGCCTTACAGGT  
CTCCATTTTGTGGTAAAAAAGTTTTAGGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACT  
TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG  
AAACCTCCGTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCA  
GCTACTCGGGAGGCTGAGGCAGGAGATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGA  
GATCGGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAACAA  
AAGATTTTATTAAAGATATTTTGTTAACTC

## FIGURE 10

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLEFWTL  
 NWVLALGQCVLAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL  
 EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGNFCVSAKNAFMLLMRN  
 IVRVVLDKVTDLLLFFGKLLVVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY  
 VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKNEAPPDNKKRKK

### Important features:

#### Transmembrane domains:

amino acids 57-80 (type II), 110-126, 215-231, 254-274

#### N-glycosylation sites.

amino acids 16-20, 27-31, 289-293

#### Hypothetical YBR002c family proteins.

amino acids 276-288

#### Ammonium transporters proteins.

amino acids 204-231

#### N-myristoylation sites.<sup>1</sup>

amino acids 60-66, 78-84

#### Amidation site.

amino acids 306-310

# **FIGURE 11**

GCCCCGCGCCCGGCGCCGGGCGCCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGAGCCTGC  
TCCCTGCTCAGCTGCGCGTCTCTGCCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCTGCTGCCCCGC  
CAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCTCTTCTGCGGGTGCTGGTGTCCA  
TCATTATGCTGAGCCCGGCGTGGAGAGTCAGCTCTACAAGCTGCCCTGGGTGTGTGAGGAGGGGGCC  
GGGATCCCCACCGTCTGCAGGGCCACATCGACTGTGGCTCCCTGCTTGGCTACCGCGCTGTCTACCG  
CATGTGCTTCGCCACGGCGGCCTTCTTCTTCTTTTTTACCCTGCTCATGCTCTGCGTGAGCAGCA  
GCCGGGACCCCCGGGCTGCCATCCAGAATGGGTTTTGGTCTTTAAGTTCCTGATCCTGGTGGGCCTC  
ACCGTGGGTGCCCTTCTACATCCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCTGTGG  
CTCCTTCCCTCTTCATCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGT  
GGCTGGGCAAGGCCGAGGAGTGCGATTCCCGTGCCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTC  
TTCTACTTGCTGTGATCGCGGCGGTGGCGCTGATGTTTATGTACTACACTGAGCCAGCGGCTGCCA  
CGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCTGTGTCTCTGC  
CCAAGGTCCAGGACGCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTTCATCACCCTCTACACCATG  
TTTGTCACTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTGCAACCCAGCT  
GGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAGACCCAGTGGTGGGATGCCCGAGCATTG  
TGGGCCTCATCATCTTCTCTCTGTGCACCCTCTTCATCAGTCTGCGCTCCTCAGACCACCGGCAGGTG  
AACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGT  
GGCAGCCTGTGAGGGCCGGGCCTTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCC  
ACTTCTGCCTGGTGTGCGCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAG  
ACCCGGAAGATGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCT  
CCTCTACCTGTGGACCCTGGTAGCCCCACTCCTCTGCGCAACCGCGACTTCAGCTGAGGCAGCCTCA  
CAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTC  
CCCACACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTGCCCCCTGAGCCGGGC  
CTTCTAGTCGTAGTGCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCAC  
ACCCACACGGGTGGAGCTGCCTCTTCTTCCCTCCTCCCTGTGCCCCATACTCAGCATCTCGGATGAA  
AGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGAACTCCCACCACAG  
TGGGGCATCCGGCACTGAAGCCCTGGTGTCTTGGTACGTCCCCCAGGGGACCTGCCCCCTTCTG  
GACTTCGTGCCTTACTGAGTCTTAAGACTTTTTCTAATAACAAGCCAGTGCCTGTAAAAAAA

## FIGURE 12

MGACLGACSLSCASCLCGSAPCILSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVESQL  
YKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRDPRAAIQ  
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFLFILIQLVLLIDFAHSWNQRWLKAE  
ECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVSIAAVLPKV  
QDAQPNSGLLQASVITLYTMFVTSALSSIQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI  
VGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQVAAACEGRAFDNEQDGVITYSY  
SFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVWKICASWAGLLLYLWTLVAPLLLRNRD  
FS

### Signal sequence:

amino acids 1-20

### Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444



## FIGURE 13

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCACCCGTTAAGGTGTCTTCTCTTTAGGGATGGTGA  
GGTTGGAAAAAGACTCCTGTAACCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAGAACG  
CTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCACACAA  
CTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC  
TTTCTGTTTGTGTTGTACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATAGAGTTAAATG  
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT  
TTTGATATATTTCTTCTGGCAGTTTTTCGATTTAAAGTGTTAATACTTGCATATGCTGTGTGCAG  
ACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTTTACTAGCAAAAG  
TGATCCTTTTCGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTGCCCATCATTTTCATTATC  
CTTGCCCTGGATTGAGACGTGGTTCCTGGATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAA  
CAGACTCCTGATAGTTCAGGATGCTTCAGAGAGGGCAGCACTTATACCTGGTGGTCTTTCTGATG  
GTCAGTTTTATTCCCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT  
GAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTAAATGTGAAAAACCCTCACAGAAAGTC  
ATCGAGGCAAAAAGAGGCAGGCAGTGGAGTCTCCCTGTCGACAGTAAAGTTGAAATGGTGACGTC  
CACTGCTGGCTTTATTGAACAGCTAATAAAGATTTATTTATTGTAATACCTCACAAACGTTGTAC  
CATATCCATGCACATTTAGTTGCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTCATCCTCTCT  
TCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAGAAAGTCTTGTGCTGTATTCTTAATC  
AAAAGACTTAATATATTGAAGTAACACTTTTTTAGTAAGCAAGATACCTTTTTATTTCATTCAC  
AGAATGGAATTTTTTTGTTTCATGTCTCAGATTTATTTTGTATTTCTTTTTTAACACTCTACATT  
TCCCTTGTTTTTTAACTCATGCACATGTGCTCTTTGTACAGTTTTAAAAAGTGAATAAAATCTG  
ACATGTCAATGTGGCTAGTTTTATTTTCTGTTTTGCATTATGTGTATGGCCTGAAGTGTGGA  
CTTGCAAAAGGGGAAGAAAGGAATTGCGAATACATGTAAAATGTCACCAGACATTTGTATTATTT  
TTATCATGAAATCATGTTTTTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGC  
ACAAAATGACTTAAACCATTCATATCATGTTTCCTTTGCGTTCAGCCAATTTCAATTAAAATGAA  
CTAAATTAAAAA

## **FIGURE 14**

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF  
 VTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT  
 AVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLQPQAEENRLLIVQDASER  
 AALIPGGLSDGQFYSPPESEAGSEEAEKQDSEKPLLEL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 54-72, 100-118, 130-144, 146-166

**N-myristoylation sites.**

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

**FIGURE 15**

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTGAGG  
 CCGCGGGCTGCCCCGCGGCTCCCTGCGCCGCGCCGCTCCCGGGACAGAAGATGTGCTCCAG  
 GGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGGGCTGCCCAT  
 CCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGGACCACGGTGCCC  
 CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGC  
 AGGCAGCTTTGCCGGCTGCCGGGCTGCAGCTCCTGGACCTGTCACAGAACCAGATCGCCAGCC  
 TGCCACGCGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTGGACCTGACGGCCAACAGGCTG  
 CATGAAATACCAATGAGACCTTCCGTGGCCTGCGGCGCTCGAGCGCTCTACCTGGGCAAGAA  
 CCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGCTCGACCGCTCCTGGAGCTCAAGCTGC  
 AGGACAACGAGCTGCGGGCACTGCCCCGCTGCGCTGCCCCGCTGCTGCTGCTGGACCTCAGC  
 CACAACAGCCTCCTGGCCTGGAGCCCGCATCCTGGACACTGCCAACGTGGAGCGCTGCGGCT  
 GGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACC  
 TGGATGTTCGGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCTGACG  
 CGCCTGCGGCTGGCCGGCAACACCCGCTTGGCCAGCTGCGGGCCGAGGACCTGGCCGGCCTGGC  
 TGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCC  
 TCTTCCCCCGCTGCGGCTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGC  
 TGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTCACTGGCCAGCCCTGAGGAGACGCGCTGCCA  
 CTTCCCCGCCAAGAAGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCCAG  
 CCACCACCACACAGCCACAGTGCCCAACACGAGGCCCGTGGTGCGGGAGCCCCACAGCCTTGCT  
 TCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCAGGCCCGCCCTC  
 CACTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCA  
 ATGGGGGACATGCCACCTGGGGACACGGCACCACTGGCGTGTGTGTGCCCGGAAGGCTTCACG  
 GGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGGCCAGCCCTACACAGTCAACGCCGAG  
 CCCACCAGGTCCCTGACCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGGTGGGGCTGC  
 AGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTACCTATCGCAACCTATCG  
 GGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACAGGTACCCCA  
 GCTGCGGCCCAACGCCACTTACTCCGTCTGTGTCACTGCTTTGGGGCCCGGGCGGGTGCCGGAGG  
 GCGAGGAGGCTGCGGGGAGGGCCATACACCCAGCCGTCCACTCCAACCACGCCCCAGTCACC  
 CAGGCCCGCAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGC  
 GCTGGCTGCGGTGGGGCAGCCTACTGTGTGCGGCGGGGCGGGCCATGGCAGCAGCGGCTCAGG  
 ACAAAGGCGAGGTGGGGCCAGGGGCTGGGCCCTTGGAACTGGAGGGAGTGAAGGTCCCCTTGGAG  
 CCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCC  
 ACTCATGGGCTTCCCAGGGCTGGCTCCAGTCAACCCCTCCACGCAAAGCCCTACATCTAAGCCA  
 GAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCC  
 ACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCT  
 GGGCCCTGTTCCTCTGGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCC  
 CTAACGTCCCCAGAACCGAGTGCTTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTC  
 CCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCAC  
 TCCAGGCGGACCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGC  
 GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAGGAAGATGC  
 TTTAGGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATCT  
 GGAAGATGTTTTTCAACTCAGAGACAAGGACTTTGGTTTTTGTAGACAAACGATGATATGAA  
 GGCCTTTTGTAGAAAAAATAAAGATGAAGTGTGAAA





## **FIGURE 18**

MRVRIGLTLLLCVLLSLASASSDEEGSQDES LDSKTTLTSDSVKDHTTAGRVVAGQIFLDSESEL  
 ESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHGEPCHFPLFLDK  
 EYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEAARRQMQEAEMMYQTGMKILNGSNKKSQKR  
 EAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMFEKLTEEGSPKGQTALGFLYASGLGVN  
 SSQAKALVYYTFGALGGNLI AHMVLVSRL

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 195-199, 217-221, 272-276

**Tyrosine kinase phosphorylation site.**

amino acids 220-228

**N-myristoylation sites.**

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

**Glycosaminoglycan attachment site.**

amino acids 267-271

**Microbodies C-terminal targeting signal.**

amino acids 299-303

**Type II fibronectin collagen-binding domain protein.**

amino acids 127-169

**Fructose-bisphosphate aldolase class-II protein.**

amino acids 101-119

## FIGURE 19

AATTCAGATTTTAAGCCATTCTGCAGTGGAAATTCATGAAGTAGCAAGAGGACACCATCTTCTT  
 GTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGTGCTAGG  
 CCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAATAAGATTGAAGACATCACTG  
 ATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAATTTTGAT  
 AAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTTTAAAGGCAGA  
 AACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG  
 CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTGGTGTT  
 CCCGGCGTGTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA  
 CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG  
 TTATTAATGTCTCCAGTGTGGAGGTCGCCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA  
 TATGCAGTGGAAGGTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTC  
 ATGCATTGAACCAGGATTGTTCAAAACAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC  
 TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAACAATATGGAGAAGGTTACATTGAAAAA  
 AGTCTAGACAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG  
 CATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAGATGCCAAAA  
 TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTATTGTTGAAACAGAAA  
 GCAGAGCTGGCTAATCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCTCCAGGCTATGA  
 AATTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCATTCTTATCTGCTCCAACCTGGACT  
 CATTTAGATCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT  
 CCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCT  
 GTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATGA  
 TCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTTAAGT  
 ATCATCTCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAA

## **FIGURE 20**

MLFWVLGLLILCGFLWTRKGKLIKIEDITDKYIFITGCDSGFGNLAARTFDKKG FHVIAACLTESG  
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDWLTLEDY  
REPIEVNLFGLISVTLNMLPLVKKAQGRVINSSVGGRLAIVGGGYTPSKYAVEGFNDLRRDMK  
AFGVHVSCIIEPGLFKTNLADPVKVIKKLAIWEQLSPDIKQQYGEgyIEKSLDKLKGNKSYVNMD  
LSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQKAE LANPKAV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212



**FIGURE 21**

CTGAGGCGGCGGTAGCATGGAGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCG  
 CACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTCTTCTTGGGGAAGTAAAA  
 GGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGA  
 CATTTCAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAGGCGAAGTAAATG  
 AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATTCCGT  
 CGTCATTTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTTGCAGGAGCATT  
 TTCAAACCAAGACCTTGTTTTCTGCTATTAAACCAAGTATAATAACAGAAAGCTGCTCTACTC  
 ATCGACTGGAACATTCCCTTATATAAACCTCAAAAAGGACTTTTTTCACAGGGTACCTTTAGTGGTT  
 GCCAATCTGGGCATGTCTGAACAACGGGTATATAAACTGTATCAGGTTCTGTATGTCCACTGG  
 TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGG  
 TACATAAGATAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAAGTG  
 GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTAAACGAGAAATTGA  
 GAAAAGGAGAGGAGCACAGATTCAGGCAGCAAGAGAGAAGAACATCCAAAAGACCCCTCAGGAGA  
 ACATTTTTCTTTGTGTCAGGCATTACGGACCTTTTTTCCAAATTCGAATTTCTTCATTCATGTGTT  
 ATGTCCTTTAAAAAATAGACATGTTTCTAAAAGTAGCTGTAAC TACAACCACCATCTCGATGTAGT  
 AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCAC  
 AAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTA  
 GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAAT  
 GAGCAGCCCAGAAACAGATGAAGAAATGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC  
 CTACATTTTGAATCCTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAAC  
 ATTTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTACC  
 TGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAACATCA  
 GATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAGGCTTACACAG  
 ACACATTCTTTAGAATTGGAAGAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCAGCACT  
 TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT  
 GAGACCATGTCTATTAAAAAATAAAATGGAAGCAAGAATAGCCTTATTTTCAAATATGGAAGAA  
 GAAATTTATATGAAATTTATCTGAGTCATTAAATTTCTCCTTAAGTGATACTTTTTTAGAAGTA  
 CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT  
 AAAATTTAAAAA

## **FIGURE 22**

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLEVKGEAKNSITDSQMDDVEVVYTTIDIQKYI  
PCYQLFSFYNSSGEVNEQALKKILSNVKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDL  
VFLLLTPSIITESCSTHRLEHSLYKPKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAV  
QTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA  
QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHHLVDVVDNLTL  
MVEHTDIPEASPASTPQIIKHKALDLDLDRWQFKRSRLDQDKRSKANTGSSNQDKASKMSSPET  
DEEIEKMKGFGEYSRSPTF

### **Important features:**

#### **Signal peptide:**

amino acids 1-19

#### **N-glycosylation sites.**

amino acids 75-79, 322-326

#### **N-myristoylation site.**

amino acids 184-154

#### **Growth factor and cytokines receptors family.**

amino acids 134-150

## FIGURE 23

GGCACAGCCGCGCGGGGAGGGGAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCCCAA  
GCAGCGCGCAGCGAACGCCCGCGCCGCCACACCTCTGCGGTCCCGCGGGCGCTGCCACCTTCCCTCCTTCCCC  
GCGTCCCCGCTCGCCGGCCAGTCAGCTTGCCGGGTTCGCTGCCCCGCGAAACCCGAGGTACACAGCCCGCGCTCT  
GCTTCCCTGGGCGCGCGCCGCTCCACGCCCTCCTTCTCCCTGGCCGGCGCTGGCACCAGGGACCGTTGCCTGA  
CGCGAGGCCAGCTCTACTTTTCGCCCCGCTCTCTCGGCTGCTGCGCTCTTCCACCACTCCAACCTCTTCTCC  
TCCAGTCCACTCGCTAGTCCCGACTCCGCCAGCCCTCGGCCGCTGCGTAGCGCGCTTCCCGTCCGGTCCCAAA  
GGTGGGAACGCGTCCGCCCCGCGCCGACCATGGCAGGTTTCGCTTCCCGCGCTTCTGCACTTGGCAGTGCTC  
AGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGGCAGCTTTACGTGTCCAAAGGCTTC  
AACAAGAAGATGCCCCCTCCAGAGATCAACGGTGATCATTTGAAGATCTGTCCAGGGTTTACCTGCTGCTCT  
CAAGAGATGGAGGAGAAGTACAGCCTGCAAAAGTAAAGATGATTTCAAAAGTGTGGTCAGCGAACAGTGCAATCATTTG  
CAAGCTGTCTTGCCTTACGTTTACAAGAAGTTGATGAATTTCAAAGAACTACTTGAAAAATGCAGAGAAATCCCTG  
AATGATATGTTTGTGAAGACATATGGCCATTTATACATGCAAAATTTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTG  
AAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCTCCTGGAGCGGATG  
TTCGCGCTGGTGAACCTCCAGTACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAG  
CCCTTCGAGAGATGTCCCTCGCAAATGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGTAATTCGCTCAAGGC  
TTAGCGGTTCGCGGAGATGTCGTGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTTGAAG  
ATGATCTACTGCTCCACTGCGGGGTCTCGTGACTGTGAAGCCATGTTACAATACTGCTCAAACATCATGAGAGGC  
TGTTTGGCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTA  
GAGGGTCTTTCAACATTGAATCGGTGATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGAT  
AATAGTGTCAAGTGTCTCAGAAGGTTTCCAGGGATGTGGACCCCCAAGCCCTCCAGCTGGACGAATTTCTCGT  
TCCATCTCTGAAAGTGCTTCAGTGCTCGCTTCAGACCACATACCCCCAGGAACGCCAACACAGCAGCTGGCACT  
AGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTTCTGGTCTCCCTTCCGAGCAAC  
GTTTGGCAACGATGAGAGGATGGCTGCAGGAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTAC  
CTGTTTGCAGTGACAGGAATGGATTAGCCAACCAGGGCAACAACCAGAGGTCCAGGTTGACACCAGCAAAACCAGAC  
ATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG  
GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCAGAG  
TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGCTGGTGTCCGTCTGGGGCA  
CAGGCCTACCTCCTCACTGCTTCTGCATCTTGTTCCTGGTTATGCAGAGAGAGTGGAGATTAATTTCTCAAACCTGAG  
AAAAAGTGTTTCATCAAAAAGTTAAAAGGCACCAAGTTATCACTTTTCTACCATCCTAGTGACTTTGCTTTTAAATGAA  
TGGACAACAATGTACAGTTTCTATATGTGGCCACTGGTTTAAAGAGTGTGACTTTGTTTTCTCATTCAAGTTTGGG  
AGGAAAAGGGACTGTGCATTGAGTTGGTTCCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAA  
CTATAGTTAGTTGTGATTTGTGATTTTATCACTTATTTGTTTGTATGTTTTTCTCATTTCGTTTGTGGGT  
TTTTTTTCCAACCTGTGATCTCGCTTGTTCCTTACAAGCAACAGGGTCCCTTCTTGGCACGTAACATGTACGTATT  
TCTGAAATATTAATAGCTGTACAGAAGCAGGTTTTATTTATCATGTTATCTTATTAAGAAAAAGCCCAAAAGC

$\frac{d}{dt} \left( \frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$

MARFGLPALCTLAVLSAALLAELKSKSCSEVRRRLVSKGFNKNDAPLHEINGDHLKICPQGST  
CCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGH  
LYMQNSELFKDLFVELKRYVYVGNVNL EEMLNDFWARLLERMFRLVNSQYHFTDEYLECVSKYTE  
QLKPFQDVPRKLKIQVTRAFAARTFAQGLAVAGDVVSKVSVNPTAQCTHALLKMIYCSHCRGL  
VTVKPCYNYCSNIMRGCLANQGDLDFEWNFNIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN  
MQDNSVQVSQKVFAQCGPPKPLPAGRISRSISESAFSAFRPHHPEERPTTAAGTSLDRLVTDVK  
EKLKQAKKFWSSLPNSVCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNLANQGNNPEVQVDT  
KPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG  
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

Important features:

Signal peptide:

amino acids 1-22

ATP/GTP-binding site motif A (P-loop).

amino acids 515-524

N-glycosylation site.

amino acids 514-518

Glycosaminoglycan attachment sites.

amino acids 494-498, 498-502

N-myristoylation sites.

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

Glypicans proteins.

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

## FIGURE 25

CTGCCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC  
 CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACT  
 TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA  
 TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGC  
 CAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGATTGGTTCTGAG  
 AGCCCCGAGAAGAAAATTTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCCTGTGATCATT  
 TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA  
 GCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTG  
 AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC  
 TTCTTCTCCACCTCACTCTCCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCA  
 TGTTTTTCAAGATCATTTTGTTTGTTGCTCTCTCTAGTGTCTTCTCTCTCGTCAGTCTTAGCCT  
 GTGCCCTCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCT  
 AGCTAGTGTCATTTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTT  
 AAATGTCAAAAAAAAAAAAAAAAAA

## **FIGURE 26**

MKVLISL L L L L L L P L M L M S M V S S L N P G V A R G H R D R G Q A S R R W L Q E G G Q E C E C K D W F L R A P R R K F M  
T V S G L P K K Q C P C D H F K G N V K K T R H Q R H H R K P N K H S R A C Q Q F L K Q C Q L R S F A L P L

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 27-33, 46-52

GACGCCAGCCGCTGCAGAGGCTGAGCAGGGAAGGAGCCAGTGCCTCCACAGCGGAAGCACAGCTCAG  
 AGCTGGTCTGCCATGGACATCCTGGTCCCACTCCTGCAGCTGCTGGTGCTGCTTCTTACCCTGCC  
 CCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCTGTGCAAAAGCTACTTCCCCTACCTGA  
 TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAG  
 ATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGGCTGCGGAACCGGAGC  
 CAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACTGCCTAGACCCAAATCCCCACTTTGAGA  
 AGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGGCTCCT  
 GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGTGTG  
 CTCTGTGCAGAGCCCAAGGAAGGTCTCTGCAGGAGTCCGGAGAGTACTGAGACCGGGAGGTGTGC  
 TCTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTC  
 GAGCCCACCTGGAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGA  
 GAACGCCCAGTTCTCCGAAATCCAATGGAACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTG  
 GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCC  
 TTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTTA  
GCAGAATGAGAGAAGACATTTCATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC  
 AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG  
 AAACACTAGGACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTC  
 CCAATGTTGTCCCTTTTCTTCTGTTCCCATGGTAAAGCTCCTCTCGCTTTTCTCTGAGGCTACAC  
 CCATGCGTCTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGAC  
 CCTCTCTCCCCACTACCACCTTCTTCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGG  
 ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTCTCAAATATTTTTTAATAAATAGACGAA  
 ACCACG

## **FIGURE 28**

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMVLTTPKSNRKMESKKRELFSSQIKGL  
 TGASGKVALLELGCCTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM  
 RQLADGSMDEVVCTLVLCVQSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFMWQQVFEPW  
 KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFSSKALICSFPSL  
 QLEQATHQPIYLPRLGT

**Important features:**

**Signal peptide:**

amino acids 1-23

**Leucine zipper pattern.**

amino acids 10-32

**N-myristoylation sites.**

amino acids 64-70, 78-84, 80-86, 91-97, 201-207





### **FIGURE 30**

MLLLTLLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQPRG  
EGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

## FIGURE 31

GTTGAATTCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTT  
 CCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT  
 ATTTGCATCTGTTTTGATAAATGATGTTGACACCTCCACCGAATTCTAAGTGGAATCATGTCGG  
 GAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGCTTTGGCCATGATGTTTACC  
 TTCAGATTCATCACCACCTTCTGGTTCACATTTTCATTTTCATTTGTTTATTTGGGATTGTTGTT  
 TGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA  
 CAGAAAGGGAAAATATGAAGTGCGTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGGCAGTG  
 CTGCTCGTCTTGATTTTGTTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCAC  
 AAATAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCA  
 TTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAACTGCAGGAGCTGCCAGGTT  
 ATGGAAGCGGCCAAGTGGAATATAAGCCCCCTTTCGGGCATTCCGTACATGTGGTTCGTACCATTT  
 AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAG  
 TGGTTACTTGTTATTTCAACAGAAGTAAAAATGATCCTCCTGATCATCCATCCTTTTCGTCTCTC  
 TCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAG  
 GATTCCGAGAATCATTTGTCATGTACATGAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT  
 CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC  
 AACCAGAATGCATATACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGC  
 ATTCAAAATCTTGTTCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAA  
 TTTTCTAGGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTAC  
 AATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGC  
 CCATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGATC  
 TGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA  
 AAAAGGAGCAACAAATTAAACAATGAAGGGCACAGCAGGACAAGCACTCATTAAAGGAATGAGGA  
 GGGAAACAGAAGTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATT  
 TCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTT  
 TTAAAGACCTAATAAACCTATTCTTCCTCAAAA

## FIGURE 32

MSGRDTILGLCILALALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTDNLSIE  
 LDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQPLWTFA  
 ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQMTIA  
 GAVVTCYFNRSKNPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMYMQNALKEQQHG  
 ALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD  
 FIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAHSFLSVFETVLDALFLCFA  
 VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

### Important features:

#### Signal peptide:

amino acids 1-20

#### Putative transmembrane domains:

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

#### N-glycosylation sites.

amino acids 204-208, 295-299, 313-317

#### N-myristoylation sites.

amino acids 147-153, 178-184, 196-202, 296-275, 342-348



## FIGURE 34

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG  
 CQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSLSLPRWR  
 ESFIVLESKPKKGVITYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMOQLLAVTVAVA  
 TPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTTSSQNRPRADPGIQRQDPSGAAFQKP  
 VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI  
 GPAGPLMGVVQYGDNPATHTNLKTHNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN  
 RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG  
 FYSLHVQSWFGLHKTLPVLRVCDTDLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN  
 LTKEFEISDTRIGAVQYTYEQRLFGFDKYSSKPDILNAIKRVGYWGGTSTGAAINFALEQL  
 FKKS KPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARHDSFF  
 VDEFDNLHQYVPRIIQNICTEFNSQPRN

### Important features:

#### Signal peptide:

amino acids 1-26

#### Transmembrane domain:

amino acids 181-200

#### N-glycosylation sites.

amino acids 390-394, 520-524

#### N-myristoylation sites.

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,  
 431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

#### Amidation site.

amino acids 304-308

CCGAGCACAGGAGATTGCTTCGCTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGC  
CAAACCATGTCTTTTTTCTGTTTTCAGAGTAGTTCACAACAGATCTGAGTGTTTAATTAAGCATGGAAT  
ACAGAAAACAACAAAAAATTAAAGCTTTAATTTTCATCTGGAATTCACAGTTTTCTTAGCTCCCTGGACCC  
GGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGCTCTCCGACTACTCACCCCGAGTGTA  
AAGAACCTTCGGCTCGCGTGCTTCTGAGCTGCTGTGGATGCGCCTCGGCTCTCTGGACTGTCTTCCGAGTA  
GGATGTCACTGAGATCCCTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTAC  
CTCAGCCTTCCCCACTACAATGTGATAGAACCGGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTTA  
CAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTCTTGTGCATTG  
TGGTGACCTCCCACCCCTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCT  
TGGTGGGGATATGAGGTTCTTACATTTTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTGGC  
ATTGTCTTAGAGGATGAACACCTTCTTTATGGTGACATAATCCGACAAGATTTT'TTAGACACATATAATA  
ACCTGACCTTGAAGAACATTATGGCATTGAGGTGGGTAAGTGAAGTTTGGCCCAATGCCAAGTACGTAATG  
AAGACAGACACTGATGTTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTAAACCTAAACCACTCAGA  
GAAGTTTTTACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCATATTT  
CTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTTATATAATGTCCAGAGAT  
CTGGTGCCAAGGATCTATGAAATGATGGGTACGTAAGAACCCATCAAGTTTGAAGATGTTTATGTGGGAT  
CTGTTTGAATTTATTAAGTGAACATTCATATTCAGAAAGACACAAATCTTTTCTTCTATATAGAATCC  
ATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCAAGGAGATCATCACITTT  
TGGCAGGTCATGCTAAGGAACACCACATGCCATTATTAAGCTTCACATTCTACAAAAGCCTAGAAGGACAG  
GATACCTTGTGGAAAGTGTTAAATAAAGTAGGTACTGTGGAAATTCATGGGGAGGTGAGTGTGCTGGCTT  
ACACTGAACTGAAACTCATGAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTATTAGTCAG  
CCCTTCAAAGATGATATGTGGAGGAATTAATATATAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGG  
ACCAAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAAGGGTGTTACTGAGTTATAAGCTCA  
CTAGGCTGTAAAAACAAAACAATGTAGAGTTTATTATTATGAACAATGTAGTCACITGAAGGTTTTGTGTA  
TATCTTATGTGGATTACCAATTTAAAAATATATGTAGTCTGTGTCAAAAACTTCTTCACTGAAGTTATA  
CTGAACAAAATTTTACCTGTTTTTGGTCATTATATAAGTACTTCAAGATGTTGCAGTATTTACAGTTATT  
ATTATTTAAATTAAGTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCATACAAGATAAAAAGGATAG  
TGAATCATTTCTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTATTATTGATACATCACTCCA  
TTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTTAAATATTTTACTGTGGT  
AATATAGAGAAGAATTAAGCAAGAAAATCTGAAAA

[illegible]

Important features:

amino acids 20-39

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

amino acids 239-243

amino acids 23-37

amino acids 271-277



# **FIGURE 37**

CGCTCGGGCACCAGCCGCGCAAGGATGGAGCTGGGTGCTGGACGCAGTTGGGGCTCACTTTTCTCAGCTCCTTCTCATC  
TCGTCCTTGCCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGGAATATCATGTGCGGGAGTGTGTG  
AATATGATCAGATTGAGTGCCTGCCCCGAAAGAGGGAAGTCGTGGTTATACCATCCCTTGTGTCAGGAATGAGGAGAA  
TGAGTGTGACTCCTGCCTGATCCACCAGGTTGTACCATCTTTGAAAACGCAAGAGCTGCCGAAATGGCTCATGGGGGGT  
ACCTTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTG  
GCCAGGTTCTGCGAGCCCCAAAGGGTCAGATTTTGTGGAAGCTATCCCCATAATGCTCACTGTGAATGGACATTTCATGC  
TAAACCTGGGTTTGTATCCAACCTAAGATTGTTCATGTTGAGTCTGGAGTTTACTACATGTGCCAGTATGACTATGTTGAG  
GTTCTGTATGGAGACAACCGCATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAG  
GATCCTCACTCCACGTCCTCTTCCACTCCGATGGCTCCAAGAATTTTACGGGTTTCCATGCCATTTATGAGGAGATCACAGC  
ATGCTCCTCATCCCCTTGTTCCATGACGGCAGTGGCTCCTTGACAAGGCTGGATCTTACAAGTGTGCTGCTTGGCAGGC  
TATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCTGGGGGCCAGTCAATGGGTACCAAGAA  
TAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAATTGGCACCCTGGGTGCTTCTTTTGTAACTCCTATGT  
TCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAAATGGAGAGTGGTCAGGGAACAGCCCATCTGCATAAAAGCCTGCCGA  
GAACCAAAGATTTTCAAGCTGGTGAGAAGGAGAGTTCTTCCGATGCAGGTTTCAAGGAGACACCATACACCAAGCTAT  
ACTCAGCGGCTTCAAGCAAGCAGAACTGCAGAGTGGCCCTACCAAGAAGCAGCCCTTCCCTTTGGAGATCTGCCCATGGG  
ATACCAACTCTGCATACCAAGCTCCAGTATGAGTGCATCTCACCTTCTACCGCGGCTGGGCAGCAGCAGGAGGACATGT  
CTGAGGACTGGGAAGTGGAGTGGGCGGGCACCATCTGCATCCTATCTGCGGGAAAATTGAGAACATCACTGCTCCAAAGA  
CCCAAGGGTTGCGCTGGCCGTGGCAGGCAGCCATCTACAGGAGGACAGCGGGGTGCATGACGGCAGCCTACACAAGGGAGC  
GTGGTTCTTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCCACTGTGTTACTGACCTGGGGAAG  
GTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAATTTTACCGGGATGATGACCGGGATGAGAAGACCATCC  
AGAGCCTACAGATTCTGCTATCATTCTGCATCCCAACTATGACCCCATCTGCTTGTATGCTGACATCGCCATCCTGAAGCT  
CCTAGACAAGGCCCCGTATCAGCACCCGAGTCCAGCCCATCTGCCTCGCTGCCAGTCGGGATCTCAGCACTTCTTCCAGGAG  
TCCCACATCACTGTGGCTGGCTGGAATGTCTTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGG  
TGCTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGAGTGTCACTGATAACATGTT  
CTGTGCCAGCTGGGAACCCACTGCCCCCTTCTGATATCTGCACTGCAGAGACAGGAGGCATCGCGGCTGTGCTTCCCGGGA  
CGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA  
CTGCCTTACCAAGGTGCTGCCTTTTAAAGACTGGATTGAAAGAAATATGAAAAGAACCATGCTCATGCACTCCTTGAAG  
TGTTTCTGTATATCCGTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGGCTGAAGTGTGATTGCGCTGTGAACCTGGCT  
GTGCCAGGGCTTCTGACTTCAGGACAAAACCTCAGTGAAGGGTGAGTAGACCTCCATTGCTGGTAGGCTGATGCCGCTCCA  
CTACTAGGACAGCAATTGGAAGATGCCAGGGCTTGCAAGAGTAAGTTTCTTCAAAGAAGACCATATACAAAACCTCTCCA  
CTCCATGACCTGGTGGTCTTCCCCAATTTTCAAGTTATACGAATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAG  
GCCCCTTTGGAGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCCCTT  
TGTGTACATGGCCACAGTACAGTCTGGTCTTTTCCCTCCCCATCTTGTACACATTTTAAATAAAATAAGGGTTGGCTTCT  
GAACCTACAAAAA  
AA

## FIGURE 38

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYT  
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDEFYVKGFYCAECRAGWYGGDCMRGQ  
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQII  
KRVCGNERPAPIQSIGSSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC  
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSGNE  
KRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPLHQLYSAAFSKQKLQSAPTK  
KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP  
KTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADL  
KVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR  
DLSTSFAQESHITVAGWNVLADVRSPGFKNDFLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCA  
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMLVSWSYDKTCSHRLSTAFTKVLPFKDWI  
ERNMK

### Important features of the protein:

#### Signal peptide:

amino acids 1-23

#### EGF-like domain cysteine pattern signature.

amino acids 260-272

#### N-glycosylation sites.

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

#### N-myristoylation sites.

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,  
474-480, 491-497, 638-644, 666-672

#### Amidation site.

amino acids 56-60

#### Serine proteases, trypsin family.

amino acids 489-506

#### CUB domain proteins profile.

amino acids 150-167

## FIGURE 39

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCGTGATTATTAACTGGCTTAATC  
TGAAGGTTCTCAGTCAAATCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTGCTTAAAGGAGCTTGGCTGG  
TTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAAATGAAGGCGCTTCTGTTGC  
TGGTCTTGCCTTGGCTCAGTCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCTGTATTGAGAACTCTGTA  
AAGGTGCTCCCACTACGGCTGACCAAAGATAGGAAGAGGCGCTCACAGATGGCTGTCCAGACGGCTGTGCGAGCC  
TCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCACTGCCACCCTCTCTTAATGACAGACGAGCCTGGCCTAGACA  
ACCTTGCCTACGTGCTCTCGGACAGAGGACGGGCAGCCAGCAATCAGCCCACTGGACTCTGGCCGGAGCAACCGAACTA  
GGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAAATCGAGCTTTGAGTGTCTTCGAA  
GGACAAAGAGCGGGAGTGAGTTGCCAACCATGCCAGCAGGGCAGGGAAAAATCTGAAACACCACTGCCCTGAAG  
TCTTTCAAGGTTGTACCACCTGATTCCAGATGGTGAATTAACAGCATCAAGATCAATCGAGTAGATCCAGTGAAA  
GCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCACTGGTCCATATCATTATCCAACACATTATCGTGATGGGG  
TGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTTAAAGGCTCAACGGGATGGACATCAGCAATGTCCCTC  
ACAACTACGCTGTGCGTCTCTCGCGCAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAAGTCCGCA  
GCAGGAACAATGGACAGGCCCCGGATGCCTACAGACCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCC  
CCGAGGAGCAGCTTGAATAAACTGGTGCGAAGGTGGATGAGCCTGGGGTTTTTCATCTCAATGTGCTGGATGGCG  
GTGTGGCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCA  
GCCAGAAAGTGCGGCTCATCTGATTAGGCCAGTGAAAGACGTGTTACCTCGTGTGTCGCCGAGGTTCCGGCAGC  
GGAGCCCTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCAGGGCCAGGGAGAGGAGCAACA  
CTCCCAAGCCCTCCATCTTACAACTACTTGTGATGAGAAGGTGGTAAATATCCAAAAGACCCCGGTGAATCTCTCG  
GCATGACCGTCGACAGGGGAGCATCACATAGAGAATGGGATTGCTTATCTATGTCATCAGTGTGAGCCCGAGGAG  
TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTGTGAATGTGGATGGGGTCGAACTGACAGAGGTGAGCC  
GGAGTGAGGAGTGGCATTATTGAAAGAATCATCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGC  
CCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCT  
GGGTCATGTGGCTGGAATTACCACGGTGCTTGATAACTGTAAAGATATTGTATTACGAAGAAACAGCTGGAAGTC  
TGGGCTTCTGCATTGTAGGAGCTTATGAAGAATAAATGGAACAAACCTTTTTTCATCAAATCCATTGTTGAAGGAA  
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTGCTGCAATGGTAGAAGTACATCAGGAATGA  
TACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTGGCACTT  
TTTTATAGAATCAATGATGGGTGAGAGGAAACAGAAAAATCACAAATAGGCTAAGAAGTTGAAACACTATATTATC  
TTGTCAGTTTTTATATTAAAGAAAGAAATACATTGTAATAATGTGAGGAAAGTATGATCATCAATGAAAGCCAGTT  
ACACCTCAGAAAATATGATTCCAAAAAATTAATACTACTAGTTTTTTTTTTCAGTGTGGAGGATTTCTATTACTCTAC  
AACATTGTTTATTTTTTCTATTCAATAAAAGCCCTAAACAATAAATGATTGATTGTATACCCCACTGAATT  
CAAGCTGATTAAATTTAAATTTTGGTATATGCTGAAGTCTGCCAAGGGTACATTATGGCCATTTTAAATTACAGCT  
AAATATTTTTTAAATGCATTGCTGAGAACGTTGCTTTCATCAAACAAGAATAAATTTTTTCAGAAGTTAAA

## **FIGURE 40**

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPS  
 PEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSFKKINR  
 ALSVLRRTKSGSAVANHADQGRESENTTAPEVFPRLYHLIPDGEITSIKINRVDPSESLSIRLV  
 GGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM  
 REQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVKRVDEPGVFI FNVLDGGVAYRHG  
 QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSROVRQORSPDIFQEAGWNSNGSWSPG  
 PGRSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVISRDGR  
 IKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPP  
 SDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFPIKSIVEGTPAYNDG  
 RIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **N-glycosylation sites.**

amino acids 108-112, 157-161, 289-293, 384-388

#### **Tyrosine kinase phosphorylation sites.**

amino acids 433-441, 492-500

#### **N-myristoylation sites.**

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,  
 467-473, 603-609

**FIGURE 41**

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT  
 CTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACT  
 TTCCACCTTTCTACAAATCCGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGGTGGGC  
 CACCAGTAACTACTTCGTGGGTGCCATTCAAGAGATTCCCTAAAGCAAAGGAGTTCATGGCTAATTTCC  
 ATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTT  
 GACAACTGTCCTTCTGTGTCTCCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAC  
 TTTGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCAGAGGCCGGTATCGCCCTCAGGAATGTAAAG  
 CTTTACAGAGGGTCGCATCCTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAA  
 CATCTGCATCCCTTCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGG  
 TAAAAAGTTTAATCGAGCCAACTCTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG  
 ACTGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG  
 CATCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTG  
 GGGTGTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACTACTGGGGAT  
 GGGGAGGCCAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTG  
 CCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGCAATGAGGTGAACGCAGAACG  
 GATGAAGCTCTTACACCAAGTGTCACGAGTCTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAAT  
 TAGTATCTGTGGAACACAATCCTTTATATATCAACATCACAGTGGATTCTGGTTTGGTGCATGACCC  
 TGGATCTTTTGGTGATGTTTGAAGAAGTATTCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAA  
 ATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCTTTTTGTATTTTCT  
 TAGCAGAGCTCCTGGTGATGTAGAGTATAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGAT  
 CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAGGATGACTCAAAGGATAA  
 AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATTATGGGAT  
 AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA  
 AGGTACGAAGATACAATACTGTTATTCATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGAGGT  
 GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTGGGAATGAAGA  
 GGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC  
 CTTACAGGGGAGGACCTGCCAGGTATGCCTTCCAGTGATGCCACCAGAGAATACATTCTCTATTAGT  
 TTTTAAAGAGTTTTTGTAATAATGATTTGTACAAGTAGGATATGAATTAGCAGTTACAAGTTTACAT  
 ATTAATAATAATAATATGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAAGCAAAA

## **FIGURE 42**

MGFNLTFHLSYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTILGKGKTLTN  
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH  
RNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFI FHDV  
DLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTALSREQFFKVNGFSNNYWGWWGED  
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV  
SVEHNPLYINITVDFWFGA

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 4-8, 220-224, 335-339

**Xylose isomerase proteins.**

amino acids 191-202

**FIGURE 43**

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGG  
CCGCTTGCCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCACAACAG  
ACGGGACAACCTTGCAAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCAT  
GTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCTGCGGCTGCTGTC  
ATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTGCCCGTCCCTCCCTCCC  
TTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAATGGCTGGTTCTTTGTTT  
TCCAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

MALSSQIWAACL LLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPI  
CIFCCGCCHRSKCGMCCKT

**Important features:**

**Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 58-59

**N-myristoylation site.**

amino acids 44-50

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 1-12



# **FIGURE 45**

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC  
 TCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT  
 TCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTG  
 GACCTTCAACACAACCCCTCTTGTCACCATACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA  
 ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAG  
 AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA  
 GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA  
 ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATT  
 TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCATCTC  
 CTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCGTGCAGCAGAACT  
 TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATG  
 GTCCTCCTGTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTG  
 GTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGG  
 AAACCTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT  
 AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT  
 GGAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCATGAGAATGTTA  
 TCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCA

## **FIGURE 46**

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP  
EGGTIIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK  
PKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIC  
VARNPVSERNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE  
EKKRVDICRETPNICPHSGENTYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT  
PRLFAYENVI

**Important features:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 224-250

**Leucine zipper pattern.**

amino acids 229-251

**N-glycosylation sites.**

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,  
291-295

## FIGURE 47

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGG  
 ATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCT  
 TAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTCCCAGGAAT  
 ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG  
 CTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCACAGTCATTGGTGCTC  
 TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATGTGTAATTCTCCAAGC  
 AACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTCATCCAGAATCCTTCAA  
 CTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTCAATAAACCCACCAGTAACG  
 ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGG  
 CTTATCCACTTCTCAGTATTTTTAGGTCTATTGCTTGTTGGAATTCTGGAGGTCCTGTTTGGGCT  
 CAGTCAGATAGTCATCGGTTTCCTTGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG  
 TGTAGTTTAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAAAAA

## **FIGURE 48**

MTCEGWTSCNGFSLVLLVLLLVVLAIPVLSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA  
TTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNSPSNSNANCEFSL  
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSSEENKHRLIHFSVFLGL  
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

**Important features:**

**Transmembrane domains:**

amino acids 10-31 (type II), 50-72, 87-110, 191-213

**N-glycosylation sites.**

amino acids 80-84, 132-136, 148-152, 163-167

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 223-227

**N-myristoylation sites.**

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 207-218

**TNFR/NGFR family cysteine-rich region protein.**

amino acids 4-12

## FIGURE 49

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGA  
 AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG  
 ATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTCGAACTGTGA  
CATGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGGAAGCCAATGACC  
 CATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC  
 TGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATGCAAATACAAGAG  
 CAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCCTCATCACTCCAGGCTCTGCCA  
 CTACTTGCTTGAGCACAGGACTGGCCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC  
 TCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCT  
 TTCTGATCAGGAGGCTTCTTTATGAATTAACTCGCCCCACCACCCCTCA

## **FIGURE 50**

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKS  
SQKQHSPVPEKAIPLITPGSATTC

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 36-59

**N-myristoylation sites.**

amino acids 41-47, 45-51, 84-90

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.**

amino acids 54-67

## FIGURE 51

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG  
 AGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGCAAGG  
 AGGAGACCCTGGTGGGAGGAAGAACTCTGGAGAGAGAGGGGGCTGGGCAGAGATGAAGTTCCAG  
 GGGCCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGGCCCCCTGCAGAG  
 CGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCCTGGGAGACGCCCTGA  
 GCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCCGAGGGGCAGCTGGCTCTAAAGTCAGTGAG  
 GCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAGGCAGGTTCCAGGCTTTGGCGC  
 AGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATGCTCTGGGAAACACTGGGCACGAGA  
 TTGGCAGACAGGCAGAAGATGTCATTTCGACACGGAGCAGATGCTGTCCGCGGCTCCTGGCAGGGG  
 GTGCCTGGCCACAGTGGTGCTTGGGAACTTCTGGAGGCCATGGCATCTTTGGCTCTCAAGGTGG  
 CCTTGGAGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGGACTCCGTGGGTCCACGGATACCCCG  
 GAAACTCAGCAGGCAGCTTTGGAATGAATCCTCAGGAGCTCCCTGGGGTCAAGGAGGCAATGGA  
 GGGCCACCAAACTTTGGGACCAACTCAGGGAGCTGTGGCCAGCCTGGCTATGGTTCAGTGAG  
 AGCCAGCAACCAGAATGAAGGGTGCACGAATCCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA  
 ACTCTGGGGGAGGCAGCGGCTCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAAC  
 AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAG  
 TGGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGT  
 CCTCCTGGGGATCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGA  
 CATAAACC CGGTGTGAAAAGCCAGGGAATGAAGCCCGGGAGCGGGGAATCTGGGATTCAGGG  
 CTTAGAGGACAGGGAGTTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTG  
 GAGGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGTT  
 GGTGGAGTCAATACTGTGAACCTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCTGGAA  
 GAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGAAGCTCTC  
 GCATCCCGTGACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCCACACTCCCTCCTTAA  
 AACACCACCCTCTCATCACTAATCTCAGCCCTTGGCCTTGAAATAAACCTTAGCTGCCCCACAAA  
 AA  
 AA





# **FIGURE 53**

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG  
CTGGGCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCT  
ACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAAGTCCCGCGGCTCCAGTGTTC  
CACAGCCCCAAAACGGAAGTGGTTTTGGGGTCACCTGGGCTGATCACTCCTACAGAGGAGGGC  
TTGAAGGACTCGACCCAGATGTGCGCCACCTATTCCAGGGCTTTACGGTATGGCTGGGTCCCAT  
CATCCCCCTTCATCGTTTTATGCCACCTGACACCATCCGGTCTATCACCATGCCTCAGCTGCCA  
TTGCACCCAAGGATAATCTCTTCATCAGGTTCCGAAGCCCTGGCTGGGAGAAGGGATACTGCTG  
AGTGGCGGTGACAAGTGGAGCGCCACCGTCGGATGCTGACGCGCGCCTTCCATTTCAACATCCT  
GAAGTCTATATAACGATCTTCAACAAGAGTGCACCATCATGCTTGACAAGTGGCAGCACCTGG  
CCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGGACAGTCTA  
CAGAAATGCATCTTCAGCTTTGACAGCCATTGTGAGGAGAGGCCCAGTGAATATATTGCCACCAT  
CTTGAGCTCAGTGCCTTGTAGAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTTCTGT  
ATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGAC  
GCTGTATCCGGGAGCGGCGTCGCACCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAA  
AGCCAAGTCCAAGACTTTGGATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG  
CATTGTGAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTGGAGGCCATGACACCAG  
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCAGGACCCAGAATACCAGGAGCGCTGCCG  
ACAGGAGGTGCAAGAGCTTCTGAAGGACCGCATCTAAAGAGATTGAATGGGACGACCTGGCCC  
AGCTGCCCTTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATC  
TCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAGGCATTACCTG  
CCTCATCGATATTATAGGGTCCATCACAACCCAACTGTGTGGCCGATCCTGAGGTCTACGACC  
CCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCCTTTCTCCGCA  
GGGCCCAGGAAGTGCATCGGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCTGGCGTTGAT  
GCTGCTGCACTTCCGGTTCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAATTGATCATGC  
GCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGAGTACTTTCTGAC  
CCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAACGGTGTGTCAA

## FIGURE 54

MSLLSLPWLGLRPVAMSPWLLLLLVGWSLLARILAWTYAFYNNCRRLQCFPPKRNWFWGHLG  
 LITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP  
 WLGEKILLSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI  
 SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC  
 RLVHDFDVAIRERRRRLPTQGIDDFKDKAKSKTLDIFDVLLLSKDEDGKALSDEDIRAEADTF  
 MFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR  
 LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENSKGRSP  
 LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN  
 VGLQ

**Important features:**

**Transmembrane domains:**

amino acids 13-32 (type II), 77-102

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 461-471

**N-glycosylation sites.**

amino acids 112-116, 168-172

# **FIGURE 55**

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTTGA  
 G CCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTTCTGCCT  
 TTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCATTGACGTGG  
 TACAGCCTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTTTTGCCGTGTGTCTTGC  
ATAATCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAGCTGGTGGACAGTTTT  
 GTAACATCTTCGAAACCTCTGTCTTACAGACATGTCCTTTTATCTTGACAGCAATGTGTTGCTT  
 GTGATTCGAACATTTGAGGGTTACTTTTGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA  
 GCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAATCTTCCTCATGTACCTGTTTCCTC  
 TCTGGATGTTGTCCCACTGAATCCCATGAATACAAACCTATTCAGCAACAGCAAAAAAAAAAAAA  
 AA

## **FIGURE 56**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIPFAR  
DAVKKCFVCLA

**Important features:**

**Signal peptide:**

amino acids 1-33

**Type II fibronectin collagen-binding domain protein.**

amino acids 30-72



## **FIGURE 58**

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKDLG  
 QLDFEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILKSMDKNG  
 TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMWWRHLVAGGG  
 AGAVSRTCTAPLDRLKVLQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIK  
 FMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQSSIYPMEVLKTRMALRKTGQYSGMLDCARR  
 ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNSADPGVFVLLACGTMSSTC  
 GQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV  
 VYENLKITLGVQSR

**Important features:**

**Signal peptide:**

amino acids 1-16

**Putative transmembrane domains:**

amino acids 284-304, 339-360, 376-394

**Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

**N-glycosylation sites.**

amino acids 129-133, 169-173

**Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

## FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGC  
 TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG  
 CACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTGCGCTCAGCT  
 GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACCTGACATCAAACCTTTCTGATAT  
 CGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCCAAAGATG  
 AGCTGTCGGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTGCTGATCAAGTGATAGTT  
 GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT  
 CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG  
 AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGTTCCCC  
 CAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACTTCTCGGAAGTCTCCAATAC  
 CAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTGCTGTGCTCTACAATGTTACGA  
 TCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG  
 ACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGT  
 CTCTTCTTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAAT  
 GTGCCCTTGGCCACAAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAATATTTCAC  
 CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG  
 AGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAGCAGAAGGCTCCAATATGAACAAGATAAAT  
 CTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAACTAGACAAGTGTGTTAAGA  
 GTGATAAGTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT  
 CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGC  
 TGTAAATGTTGCTCTGAGGAAGCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCAC  
 AAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG  
 GCTGCATTTTAGTAATGGGTCAAATGATTCACCTTTTATGATGCTTCCAAAGGTGCCTTGGCTTC  
 TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTAGCATAAACAGAGCAGT  
 CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 6o**

MASLGQILFWSIIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS  
DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKC  
YIITSKGGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFQPTVVWASQVDQGANFSEVS  
NTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTESI KRRSHLQLLSKASL  
CVSSFFAISWALLPLSPYLMLK

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 258-281

**N-glycosylation sites.**

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,  
220-224

**N-myristoylation sites.**

amino acids 52-58, 126-132, 188-194



## FIGURE 61

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG  
 CACCAGGAGCCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGT  
 GGGCTACCCCCTGGTGGTGGTTATGGGGGTCTGCCCTGGAGGGCCTTATGGACCACCAGCTGG  
 TGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCTCTGGAACCTCAGGAGGACCATATG  
 GCGGTGCAGCTCCCGGGGGCCCCCTATGGTCAGCCACCTCCAAGTTCTACGGTGCCAGCAGCCT  
 GGGCTTTATGGACAGGGTGGCGCCCCCTCCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC  
 GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA  
 ATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA  
 GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGGAAGAACCTCTT  
 CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC  
 AAATGGGCTACAACCTGAGCCCCCAGTTCACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCT  
 GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA  
 GGCCTTCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTCGAGGACTTCGTCA  
 CCATGACAGCTTCTCGGATGCTATTGACCCAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT  
 TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTTCTGTCCCTCTAGAAGAAC  
 ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCA  
 AATAGTGAGGACCGGGGCTGAGGCCACACAGATAGGGGCCTGATGGAGGAGAGGATAGAAGTTGA  
 ATGTCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCTTGTAAATGG  
 AGTTAGTGTCCAGTCAGCTGAGCTCCACCCTGATGCCAGTGGTGAAGTTCATCGGCCTGTTACC  
 GTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAACGAGCCCATTTTCTCCAAAGTGAAT  
 CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCTGCCACACCCATAAAT  
 CCTTGTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT  
 CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCCCTGCCATGCTCTGCTCGGCT  
 TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTTAATTTGCATTTTTTTTC  
 ATTTGGGGCCAAAAGTCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

## **FIGURE 62**

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG  
 HPNPGMFPSGTPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDS DH  
 SGYISMKELKQALVNCNWSSFNDETCIMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDR  
 DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREK  
 DTAVQGNIRLSFEDFVTMTASRML

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-  
 66, 70-75, 78-83, 83-88, 87-92, 110-115



## **FIGURE 64**

MQGRVAGSCAPLGLLLVCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGSPNSEHPQPAL  
DPRSNDLARVPLKLSVPPSDGFPPAGGSAVQRWPPSWGLPAMDSWPPEDPWQMMAAAEDRLGEA  
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRLLPRSNSLGAGGKILSQRP  
PWSLIHRVLPDHPWGTNLNPSVSWGGGGPGTGWGTTRMPHPPEGIWGINNQPPGTSGWNINRYPGGS  
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPPGVLRPPGSSWNIPAGFPNPPSPRLQWG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Casein kinase II phosphorylation sites.**

amino acids 56-59, 155-158

**N-myristoylation sites.**

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,  
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

## **FIGURE 65**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTC  
TGGGCTGCCCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA  
CTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA  
TTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCACCATGC  
AAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCATTGAAGCCTGTGTCTTCTTGGCCC  
GGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAGCAGGCCCCCACCTC  
CTGAGTGGCAATAAATAAAATTCGGTATGCTG

## **FIGURE 66**

MGSGPLVLVLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSTSVTL  
HHARSQHHVVCNT

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 37-41

**N-myristoylation sites.**

amino acids 15-21, 19-25, 60-66

## FIGURE 67

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGGC  
CAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCC  
TTCTCGGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCG  
CTGGGCCTGCCGTTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC  
AAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCCGTCCGG  
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTGGCTGTGGGGCTG  
GCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCCACTAGCGA  
GGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAAGGCT  
GCCTGCCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAA  
GGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAA  
AGACTCTGCCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACTTTTATATATTTATATAAAATTAG  
TAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

## **FIGURE 68**

MANPGLGLLLALGLPFLRLRWGRAWGQIQTTTSANENSTVLPSTSSSSDGNLRPEAITAIIVVFS  
LLAALLLAVGLALLVRKLRKQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

**Important features:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 56-80

**N-glycosylation site.**

amino acids 36-40

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 86-90

**Tyrosine kinase phosphorylation site.**

amino acids 86-94

**N-myristoylation sites.**

amino acids 7-13, 26-32



## FIGURE 69

GCCAGGAATAACTAGAGAGGAACAATGGGGTTATTAGAGGTTTGTCTTCTTAGTCTGTGCTGCTGCACCAAG  
TCAAATACTTCTTCAATTAAGCTGAATAATAATGGCTTTGAAGATATTGTCATTGTTATAGATCCTAGTGTGCCAGAA  
GATGAAAAAATAATTGAACAAATAGAGGATATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGA  
TTTTTTTTCAAAAATGTATCTATATTAATTCCTGAGAATTGGAAGGAAAAATCCTCAGTACAAAAGGCCAAAAATGAA  
AACCAATAACATGCTGATGTTATAGTTGCACCACTACACTCCCAGGTAGAGATGAACCATACACCAAGCAGTTTACACA  
GAATGTGGAGAGAAAAGCGAATACATTCACTTCAACCTTGACCTTCTACTTGGAAAAAACAAAATGAATATGGACCA  
CCAGGCAAACTGTTTGTCCATGAGTGGGCTCACCTCCGGTGGGGAGTGTGTTGATGAGTACAATGAAGATCAGCCTTTC  
TACCGTGCTAAGTCAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGGTAGAATAGAGTTTATAAGTGT  
CAAGGAGGCGAGCTGTCTTAGTAGAGCATGCAGAAATGATTCTACAACAAAATGATGGAAGAAAGATTGTCAATTTCTT  
CCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATGCAAAGTATTGATTCTGTTGTTGAATTTGTAAACGAA  
AAAACCCATATCAAGAAGCTCCAGGCTACAAAACATAAAGTGCAATTTAGAAGTACATGGGAGGTGATTAGCAAT  
TCTGAGGATTTAAAAACACCATACCCATGGTGACACCACTCCTCCACCTGTCTTCTCATTGCTGAAGATCAGTCAA  
AGAAATGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGTAAAGACCCGCTAAATCGAATGAATCAAGCAGCA  
AAACATTTCTGCTGCAGACTGTTGAAATGGATCCTGGGTGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTA  
AATAAGCTAATCCAAATAAAAGCAGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGA  
ACTTCCATCTGCTCTGGAATTAATATGCATTTCAGGTGATTGGAGAGCTACATTCCCAACTCGATGGATCCGAAGTA  
CTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTTCTTGATTGATGAAGTGAACAAAGTGGGGCCATTGTTTAT  
TTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTTTATGTT  
TCAGATGAAGCTCAGAACAAATGGCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGAA  
TCCCTTCAGCTCGAAAGTAAGGGATTAACTGAATAGTAATGCCTGGATGAACGACACTGTCAATTTGATAGTACA  
GTGGGAAAGGACACGTTCTTCTCATCACATGGAACAGTCTGCCTCCAGTATTCTCTCTGGGATCCCAAGTGAACA  
ATAATGGAAATTTACAGTGGATGCAACTTCCAAATGGCCTATCTCAGTATTCCAGGAACTGCAAGGTGGGCACT  
TGGGCATACAATCTTCAAGCCAAAGCGAACCCAGAACATTAATATTACAGTAACCTTCTCGAGCAGCAAAATCTTCT  
GTGCCTCCAATCACAGTGAATGCTAAATGAATAAGGACGTAACAGTTTCCCAGCCCAATGATTGTTTACGCAGAA  
ATTCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTCATTGAATCACAGAAATGGACATACAGAAGTT  
TTGGAATTTTGGATAATGGTGACGGCGCTGATTCTTCAAGAATGATGGAGTCTACTCCAGGTATTTACAGCATAT  
ACAGAAAAATGGCAGATATAGCTTAAAGTTTCGGGCTCATGGAGGAGCAACACTGCCAGGCTAAAATTACGGCTCCA  
CTGAATAGAGCCCGCTACATACCAAGCTGGGTAGTGAACGGGGAAATTAAGCAAAACCCGCCAAGACCTGAAATTTGAT  
GAGGATACTCAGACCACCTTGGAGGATTTCAGCCGAACAGCATCCGGAGGTGCATTTGTGGTATCACAGTCCCAAGC  
CTTCCCTTGCTGACCAATACCCACCAAGTCAAATCACAGACCTTGATGCCACAGTTTATGAGGATAAGATTATCTT  
ACATGGACAGCACCAGGAGATAATTTTATGTTGGAAAAAGTTCAACGTTATATCATAAGAATAAGTGCAAGTATTCTT  
GATCTAAGAGACAGTTTGTATGATGCTCTTCAAGTAAATACTACTGATCTGTCCACCAAGGAGGCCAACTCCAAGGAA  
AGCTTTGCATTTAAACCAGAAAAATATCTCAGAAGAAAAATGCAACCCACATATTTATGCCATTAAAGTATAGATAAA  
AGCAATTTGACATCAAAAGTATCCAACATTGCACAAGTAACTTTGTTATCCCTCAAGCAAAATCCTGATGACATTGAT  
CCTACACCTACTCCTACTCCTACTCCTACTCCTGATAAAAGTCATAATTTGGAGTTAATTTTCTACGCTGGTATTG  
TCTGTGATTGGGTCTGTTTAATTGTTAACTTTATTTAAGTACCACCATTTGAACCTTAACGAAGAAAAAATCTTC  
AAGTAGACCTAGAAGAGAGTTTAAAAAACAAAACAATGTAAGTAAAGGATATTTCTGAATCTTAAATTCATCCCAT  
GTGTGATCATAAACTCATAAAAAATAATTTAAGATGTGGAAGGAGGATACTTTGATTAAATAAAACACTCATGGATA  
TGTAATAACTGTCAAGATTAATAATTAATAGTTTCAATTTATTTGTTATTTATTTGTAAGAAATAGTGATGAACAAAG  
ATCCTTTTTCATACTGATACCTGGTTGTATATTATTTGATGCAACAGTTTCTGAAATGATATTTCAAATTTGCATCAA  
GAAATTAATAATCATCTATCTGAGTAGTCAAATACAAGTAAAGGAGAGCAATAAACAACATTTGAAAAAATAAAAAA  
AA

## FIGURE 70

MGLFRGFVFLVLCLLHQSNTSFIKLNNGFEDIVIVIDPSVPEDEKIEQIEDMVTASTYLFE  
 ATEKRFFFKNVSIIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEY  
 IHFTPDLLLGGKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISAGISGRN  
 RVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDQVTEKASIMFMQSIDSVVEFCNEKTHNQEAP  
 SLQNIKCNRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLVLDKSGSMGGKDRNLNR  
 MNQAAKHFLLOTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTICSGIK  
 YAFQVIGELHSQLDGSEVLLLTGDNNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGG  
 SHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTNSNAWMNDTVIIDSTVGKDTFFL  
 ITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR  
 AANSSVPPITVNAKMNDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGA  
 GADSFKNDGVYSRYFTAYTENGYSKVRAGGANTARLKLRLPPLNRAAYIPGWVVNGEIEANPP  
 RPEIDEDTQTTLEDFSRASGGAFVVSQVPSLPLPDQYPPSQITDLDTVHEDKIIILTWTAPGDN  
 FDVGKVQRYIIRISASILDRLDSFDDALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAI  
 KSIDKSNLTSKVSNIQVTLFIPQANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVI  
 VNFILSTTI

### Signal peptide:

amino acids 1-21

### Putative transmembrane domains:

amino acids 284-300, 617-633

### Leucine zipper pattern.

amino acids 469-491, 476-498

### N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

## FIGURE 71

CTCCTTAGGTGGAAACCTGGGAGTAGAGTACTGACAGCAAGACCGGGAAAGACCATACGTCCTCCCGGGCAGGGGTGA  
CAACAGGTGTATCTTTTATGATCTCGTGTGGCTGCCTTCTATTTCAAGGAAAGACGCCAAGGTAATTTGACCCA  
GAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCAAGTTATGCCAGGATTTACTAGAGAGTGTCA  
ACTCAACAGCAAGCGGCTCCTTCGGCTTAACCTGTGGTGGAGGAGAGAACCTTTGTGGGGCTGCGTTCTCTTAGCA  
GTGCTCAGAAAGTGACTTGCCTGAGGGTGGACCAAGAAAGGAAAGGTCCTTCTGCTGTTGGCTGCACATCAGGAA  
GGCTGTGATGGGAATGAAGGTGAAACTTGGAGATTTCACTTCAGTCATTGCTTCTGCTGCAAGATCATCTTTAAA  
AGTAGAGAAAGCTGCTCTGTGTGGTGGTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAGCAGCTC  
CGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCAGGGAAAGCCCTTCCGTGGGGGGCCCCGGCTTTGAGGGATGCC  
ACCGGTTCTGGACGCATGGCTGATTCCTGAATGATGATGTTTCGCGGGGGGCTGCTTGGCTGGATTTCCTGGGTGGT  
GTTTGTCTGGTCTCCTCTGTGTGCTATCTGTCTGTACATGTTGGCTGCACCCCAAGGTGACGAGGAGCAG  
CTGGCACTGCCAGGGCCAAACAGCCCAAGGGGAGGAGGGGTACAGGCCCTCTCAGGAGTGGGAGGAGCAGCAC  
CGCACTACGTGAGCAGCTGAAGCGGCAGATCGCAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGCAGAGCTCAGG  
AATGGGCACTACCAAGCCAGCGATGCTGCTGGCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCACCTC  
CTGGCCCTTCTGCACTCGCAGGTGGCAAGGCAGAGGTGAATGCTGGCTCAAGCTGGCCACAGAGTATGCAGCAGTG  
CCTTTTCATAGCTTTACTCTACAGAAAGGTGTACAGCTGGAGACTGGCTTACCCGCCACCCCGAGGAGAAAGCTGTG  
AGGAAGGACAAGCGGGATGAGTTGGTGGAAAGCCATTGAATCAGCCTTGGAGACCTTGAACAATCCTGCAGAGAACAGC  
CCCAATCACCGCTCCTTACAGCGCTCTGATTTATAGAAAGGATCTACCGAAGAGAAAGGGACAAGGGGACATTTGAT  
GAGCTCACCTTCAAAGGGGACCAACAAACAGAACTCAAACGGCTCATCTATTTCGACCATTCAGCCCATCATGAAA  
GTGAAAAATGAAAGCTCAACATGGCCAAACAGCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGGTGGCAAGTTC  
CGGAGTTTATGCAGAAATTCAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGG  
AAAGAGAAATAAATGAAGTCAAAGGAATACTTGAAACACTTCCAAAGCTGCCAACTTCAGGAACCTTACCTTCATC  
CAGCTGAATGGAGAAATTTCTCGGGGAAAGGCACTTGATGTTGGAGCCCGCTTCTGGAAGGGAAGCAACGTCTTCTC  
TTTTCTGTGATGTGGACATCTACTTCACTCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAGAAAG  
GTATTTTATCCAGTTCTTTTCACTCAGTACAATCTGGCATAATATACGGCCACCATGATGCACTCCCTCCCTTGGAA  
CAGCAGCTGGTCATAAAGAAAGGAACTGGATTTTGGAGAGACTTTGGATTTGGGATGACGTGTGATGATCGGTGAGC  
TTCATCAATATAGGTGGGTTTGTCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTC  
CACAGCAACCTCATAGTGGTACGGACGCTGTGCGAGGACTCTTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAG  
CTGACCCCGAGCAGTACAAGATGTGCATGCACTCAAGGCGCATGAACGAGGCATCCACGGCCAGCTGGGCACTGCTG  
GTGTTCAAGCACGAGATAGAGGCTCACCTTCGCAACAGAAACAGAAAGCAAGTAGCAAAAAAACAATCACTCCCA  
GAAGGATTGTGGGAGACACTTTTTCTTTCTTTTGAATTACTGAAAGTGGCTGCAACAGAGAAAAGACTTCCATAAA  
GGACGACAAAAGAAATGGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTCTGTTGGGCTTTTACAAACAGA  
AATCAAAATCTCCGCTTTGCCTTGCAAAAGTAACCCAGTTGCACCTGTGAAGTGTCTGACAAAGGCAGAAATGCTGTG  
AGATTATAAGCCTAATGTTGGAGGTTTGTGTTGTTTACAATACACTGAGACCTGTGTTTGTGTGCTCATTGA  
AATATTATGATTTAAGAGCAGTTTGTAAAAAATTCATTAGCATGAAAGGCAAGCATATTTCTCTCATATGAATGA  
GCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAAAATATCAGAAGGCAGGAGAGGAGATAGGCTTATTATGATAGT  
AGTGAGTACATTAAAGTAAATAAATGAGCAGAGAAAGAAAGAAACATAAATATCGTGTATATTTTCCCAAGAT  
TAACCAAAAAATATCTGCTTATCTTTTGGTTGTCTTTTAACTGTCTCCGTTTTTTCTTTTATTTAAAAATGCACT  
TTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCACTTTGCAAGCCTTACAAGAGAGCAAGTGTGGCTAC  
ATTTTATATTTTAAAGAGATCTTTGAGATGATTTATGAGAACTTTCAGTTCAAAGCATCAAATTTGATGCCATAT  
CCAAGGACATGCCAAATGCTGATTCTGTGAGGCACTGAATGTGAGGCACTGAGACATAGGGAAGGAATGGTTTGTACT  
AATACAGACGTACAGATACTTTCTCTGAAGAGTATTTTGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATGAC  
ACTTTCTGCTTACAGAAAAGGAAACTCATTCAGACTGGTGATATCGTGATGACCTAAAAGTCAGAAACCACATTTT  
CTCCTCAGAGTAGGGACCGCTTCTTACCTGTTTAAATAAACCAAGTATACCGTGTGAACCAACAATCTCTTTT  
AAAACAGGGTCTCCTCTGCTTCTGCTTCCATAAGAAGAAATGGAGAAAATATATATATATATATATATATTGT  
GAAAGATCAATCCATCTGCCAGAACTAGTGGGATGGAAGTTTTGCTACATGTTATCCACCCAGGCCAGGTGGAAG  
TAACTGAATTTTAAAAATTAAGCAGTTCTACTCAATCACCAGATGCTTCTGAAAAATGCAATTTATACCATTT  
CAAATATTTTAAAAATAAATACAGTTAACTAGAGTGGTTTCTTCACTCATGTGAAATTTATAGCCAGCACCAG  
ATGCATGAGCTAATATCTCTTTGAGTCTTCTGCTTCTGTTGCTCAGTAAACTCATTTGTTAAAAAGCTTCAAGAC  
ATTCAAGCTGTTGGTGTGTTAAAAATGCATTGATTTGATTTGACTGGTAGTTTATGAAATTAATTAACACAGG  
CATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA





## **FIGURE 74**

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTDFDLPALQ  
PHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGSEHQINSEAT  
FAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP  
FNLRELLPKQLGQYFRYNGSLTTPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLV  
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS  
VVFTSAQATTEA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

## FIGURE 75

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGTGTC  
TCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAAATGTCTACA  
ATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTTCATCACAA  
ATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGTCTGACAGCTCC  
AGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCTGA  
AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCAC  
ACGCTGGTGTCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTTCGTCCC  
AGGGCCCCCTCGCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT  
CAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGTGTTCCTTTTT  
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAATTT  
GATTTTGATTTATGAAATGAATTTGACAAAAGATTCTTTGTGCTGTGAAAAAATCGTGATTA  
ACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGA  
AAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA  
GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAAATTTTTGTGACTCTGAAG  
AAAACACGGAAGGTACTTCTCTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCGGATAAA  
ACAGTCATTGAATATGAATATGATGTCAGAACCACTGACATTTGTGCGGGGCCTGAAGAGCAGGA  
GCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAG  
TCTTGGGCCCCGAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTGGCG  
CAGGAGCACACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCTGACTGGGA  
TCCCCAACTGGCAGGCTGTGTATTCCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCG  
AGCCTTCTGAGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCT  
CCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGTTATA  
TGTGCAGATGGAAAACTGATGCCAACACTTCCTTTGCCTTTTGTTCCTGTGCAACAAGTGAG  
TCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTGAGTGT  
CTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTGGTTCATGCATGTA  
GGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGTTGTTCTATGCAGAGAA  
AGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGGTGGGTGT

## **FIGURE 76**

MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSI  
SVVLTAPEKWKRNPEDLPVSMQQIY  
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLK  
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYIGNEFDKRFFVPAEK  
IVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC  
DSEENTEGTSLTQQESLSRTIPDKTVIEYDYVRTTDICAGPEEQELSLQEEVSTQGTLLSQ  
ALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSSFDQDS  
EGCEPSEGDGLGEEGLLSRLYEAPDRPPGENETYLMQFMEEWGLYVQMEN

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426



## FIGURE 77

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC  
 CTGGGAAGATGGCCGGCCCGTGGACCTTACCCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATC  
 CAAGCCACCCTCAGTCCCCTGCACTGCACTTCTCATCCTCGGCCCAAAAGTCATCAAAGAAAAGCTGAC  
 ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC  
 GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCCTGAAGCACATC  
 ATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCA  
 GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTGGTCAAGACCA  
 TCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGCC  
 CCCACCCGCTGGTCCCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTCTGTGA  
 TAAGCTCTCCTTCCCTGGTGAACGCCTTAGCTAAGCAGGTGATGAACCTCCTAGTGCCATCCCTGC  
 CCAATCTAGTGAAAAACCAGCTGTGTCCCGTGATCGAGGCTTCCCTCAATGGCATGTATGCAGAC  
 CTCTGCAGCTGGTGAAGGTGCCATTTCCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTGA  
 TCCTGCCATCAAGGGTGACACCATTGAGCTCTACCTGGGGGCAAGTTGTTGGACTCACAGGGAA  
 AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCG  
 TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA  
 ATTCATGGTCTGTGGACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC  
 TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC  
 ACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTT  
 TCCCTCCAGTGAAGCCCTCCGCCCTTGTTCACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT  
 TTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG  
 ATGAACCTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA  
 CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTGAAGG  
 CCTTGGGATTCGAGGCAGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCC  
 TTGTGGAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGATGGCAGCCATCAGGGAAGGCTGG  
 GTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTG  
 CCTGTGAAAAA

## **FIGURE 78**

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIEKLTQELKDNATSILQQLPLLSAMREK  
 PAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIIVE  
 FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL  
 VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYLGAKLLDSQGKVT  
 KWFNNSAASLTMPITLDNIPFSLIVSQDVVKAABAVALSPEEFMVLLDSVLPESAHLKSSIGLIN  
 EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALRPLFTLGIEASSEAQFYT  
 KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSGVPVSLVKALG  
 FEAAESSLTKDALVLTPASLWKPSSPVSQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457





## FIGURE 81

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTT  
 CCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCCTGCCCTCCTTTCCCT  
 GCCCACCGCTGCTTCTGCGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG  
 GTTGATCTGTGGCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTTCCTCCCGACTCCGCTCCCGG  
 ACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCTCTCCTCCTTGCTGGGA  
 CTCGCGCTGCTCTGGTTCCCCCTGGACTCCACGCTCGAGCCCGCCAGACATGTTCTGCCTTTT  
 CCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCTGATGT  
 ACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCT  
 GTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACAC  
 TCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCCAGCACAAACGGGACCATGTACCAACACGGAG  
 AGATCTTCAGTGCCCATGAGCTGTTCCCTCCCGCTGCCCAACCAGTGTGTCTCTGCAGCTGC  
 ACAGAGGGCCAGATCTACTGCGGCCTCACAACTGCCCCGAACAGGCTGCCAGCACCCCTCCC  
 ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAAGCAATCGGATGAAGAGGACA  
 GTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGTGGGAGAAAG  
 AGAGGCCCGGGCACCCAGCCCCACTGGCCTCAGCGCCCCCTCTGAGCTTCATCCCTCGCCACTT  
 CAGACCCAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCT  
 GTGTGCATGGCGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC  
 CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC  
 CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCCAGAGG  
 ACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGTC  
 CTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGC  
 CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAGAGAG  
 GTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAG  
 GAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCACGAAGGTCACT  
 GGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTACGGCCAGTCCAGACAAAGTGACCAAG  
 ACATAACAAAGACCTACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTAATAAA  
 TAAGAAGTGCATTACCTCAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 82**

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSE  
 GAHVSCYRLHCPVHCPQPVTEPQQCCPKVEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELF  
 PSRLFNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR  
 HPQDPCSSDAGRKRGPPTAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKKACVHGGKTY  
 HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTFYPCRHPKVAGKCKICPEDKADPGHSE  
 ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH  
 SQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPGAEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

# **FIGURE 83**

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAGAGCCTCTCC  
 GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCATCCGTCACCTCTCCTGTCA  
 TCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTTGGTTCTGAGTC  
 TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTTGGGCCAGACAAGCCTGTCCAGGCCTGGTGGGGAG  
 GACGCAGCATTTCTCTGTTCCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGTTCTTCAGGGG  
 CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGAAGGACCAGCCATTATGCAGATGCCACAGTATC  
 AAGGCAGGACAAACTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAACATTACT  
 GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCAGTCTTACTACCAGAAGGCCATCTGGGAGCT  
 ACAGGTGTCAGACTGGGCTCAGTTCTCTCATTTCATCACGGGATATGTTGATAGAGACATCCAGCTAC  
 TCTGTCAGTCTCGGGCTGGTTCCTCCGCGCCACAGCGAAGTGGAAGGTCCACAAGGACAGGATTTGTCC  
 ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAA  
 CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG  
 GAGATACCTTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTA  
 TTTTTTGGCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCAGTGGAAAATCCAGGCGGAACTGGACTG  
 GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAG  
 AGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAATGTAACCCATAGAAAAGTCCCCAGGAGGTG  
 CCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAACATTA  
 CTGGGAGGTGGACGGAGGACACAATAAAGGTGGCGGTGGGAGTGTGCCGGATGATGTGGACAGGAGGA  
 AGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTC  
 ACATTAAATCCCGTTTATCAGCGTCTTCCCAGGACCCACCTACAAAATAGGGGTCTTCTCTGGACTA  
 TGAGTGTGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTATACCTGACATGTCGGTTTG  
 AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAATCCCATAGTCATCTGC  
 CCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGCAATCCAGAGACAAGCAACAG  
 TGAGTCTCTCTACAGGCAACCACGCCCTTCTCCCCAGGGGTGAAATGTAGGATGAATCACATCCACAT  
 TCTTCTTTAGGGATATTAAGGTCTCTCTCCCAGATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCA  
 GATGAAGGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAG  
 CTGACATTACATTTAGTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAG  
 AACCGTCAGGAATCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAG  
 ATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTAAAAAA





## FIGURE 85

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCCAGACATGCTGCTGCTGCTGCTGCCCCCT  
GCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTCCGTGA  
CGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCATGGCTGGATT  
TACCCTGGCCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGACCAGGATGCTCC  
AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACCGATTCCACCTCCTTG  
GGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGAAGAAGTGATGCGGGGAGA  
TACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCTGTGAA  
TGTGACAGCCTTGACCCACAGGCCCCAACATCCTCATCCCAGGCACCCTGGAGTCCGGCTGCCCCC  
AGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATA  
GGGACCTCCGTGTCCCCCTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCCCTCATCCACA  
GCCCCAGGACCATGGCACCAGCCTCACCTGTGAGGTGACCTTCCCTGGGGCCAGCGTGACCACGA  
ACAAGACCGTCCATCTCAACGTGTCTACCCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGA  
GACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCT  
GCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGA  
GAGGCCTGACCCTGTGCCCCCTCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCAC  
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCT  
GAACGTCTCCCTGCAGAGCAAAGCCACATCAGGAGTGAAGTCAAGGGGTGGTGGGGGAGCTGGAG  
CCACAGCCCTGGTCTTCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAA  
TCGGCAAGGCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTGAGGGGTTT  
AGCCTCTCAGGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAG  
CTTCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGTG  
AAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG  
ATGAGAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGAGAAGTCA  
GAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATG  
TGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCC  
TCCCTTTTATTTTTTAACTAAAAGACAGACAAATTCCTA

## **FIGURE 86**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYPSHGWIYPGPVVHGYWFREG  
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY  
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVFWACEQGTTPMISWIGTSVSPDPSTTRS  
SVLTLPQPQDHGTS LTCQVTFPGASVTNKTVHLNVSYPQNLMTVFQGDGTSTVLGNGSSL  
SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP  
LGSQQVYLNVSLSKATSGVTQGVVGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGD TGIE  
DANAVRGASQGPLTEPWAEDSPDQPPFASARSSVGEGELQYASLSFQMPWDSRGQEATDTE  
YSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

## FIGURE 87

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC  
 CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC  
 TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT  
 TCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTTGA  
 TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCTGTGACATGACCTCTG  
 GGGGTGGCGGCTGGACCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG  
 GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC  
 CAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACT  
 ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCAATAAGTCCCCCATGCAGCACTGG  
 AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCT  
 GTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC  
 CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCAGAAAACAGCATCTTATTACTCACCTAT  
 GGCCAGCGGGAATTCAC TGCGGGATTTGTT CAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAA  
 CGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG  
 GATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT  
 GGAACATCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG  
 TTGAGAGTTTTGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAA  
 CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGA  
 AAAAAA

**FIGURE 88**

MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI  
 YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAT  
 SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYG  
 EGKCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRVFNNERAANALCAGMRVTGCN  
 TEHHCIGGGGYFPEASPQCGDFSGFDWSGYGTHVGYSRSSREITEAAVLLFYR

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation site.

amino acids 163-167

Glycosaminoglycan attachment sites.

amino acids 74-78, 289-293

N-myristoylation sites.

amino acids 76-82, 115-121, 124-130, 253-259, 292-298



**FIGURE 90**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFA  
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVTEMALFV  
TVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

**FIGURE 91**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC  
 TCGCTGCTGCTTCGTGTTCCCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATG  
 GTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT  
 CGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCT  
 GGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCGAACCACAGCCCCC  
 CACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG  
 GCCCTGAACCTGCTCGTCACAGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT  
 CCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAG  
 AGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG  
 GAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTG  
 CTCCCGAGACCAGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTG  
 TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCCAGATTACAACTAC  
 CATAGTGATAACCCCTACTACCCATCTGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGC  
 TGGAAGGACAGGCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCTC  
 AGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG  
 AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGG  
 AGGAGGAGTGGGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGG  
 TCCCCGAGGCCTGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC  
 CCTTGGTTCTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACA  
 GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGG  
 GCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTGTCTGTGTGCTGAGCATGG  
 CATGAGGCTGAAGTGGCAACCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC  
 CAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG  
 GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATC  
 CGCGTGCTGTGTGTCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCG  
 GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTGACACGGGGTCTCCCGGATCTGGATGGCGC  
 CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGCCGAGAGCATGTGCTGGATCTGTTC  
 TGTGTGTCTGTCTGTGGGTGGGGGGAGGGGAGGGAAGTCTGTGAAACCGCTGATTGCTGACTTT  
 TGTGTGAAGAATCGTGTTCTTGAGCAGGAAATAAAGCTTGCCCCGGGGCA

## **FIGURE 92**

MQLTRCCFVFLVQGSLLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL  
 LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF  
 SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGRRTSLCTHDP  
 AKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71



## FIGURE 93

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCCTGCGCTCGCC  
 CTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGCTTTCTT  
 CTGGTTGGTGTCTCTACTGATTTTCGTCCTTGTGTTGGTTCATGGCAAGAGTCATTATTGACAACA  
 AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTGTCTCTGTCTATATCCAAGAA  
 ATGTTCCGATTTCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTGAAGAGTATAAACCC  
 AGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGGGCTTTGGAATCATGA  
 GTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTTCAT  
 GGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGT  
 ATTCTGGGGCATTGTATTTTTGATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTC  
 TCCTGACCCACCTGCTGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG  
 TCAGCATTTATAATCCTGGTGTCTATGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG  
 AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGAT  
AACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCT  
 TTTTCTGAAAATCCCTTTTCTGGTGAATTGAGAAAGAAATAAACTATGCAGATA

## FIGURE 94

MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG  
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV  
FSFVNTLSDSLGPGTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKKWGILLIVLLT  
HLLVSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSCLKCLLCQDKNFLLYNQSR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65



**FIGURE 96**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQSNQVFPSLSLIPLTQM  
LTLGPDHLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**  
amino acids 1-16

## FIGURE 97

GCTCAAGTGCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT  
 CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTGACCATG  
 GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGCCAGCCTGC  
 AGAGCTGTCTGTGAAGTTCCAGAAAATATGGTGGAAATTTCCCTTTATACCTGACCAAGTTGC  
 CGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGAGGGGACTCAGGCAAGGCAACTGAG  
 GGCCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAGGGCCCTGGACCGAGAGGA  
 GCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATGGACATGTCTTGTGGGGTCCAC  
 AGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTGCCCCATTTCTCTCAAGCCATCTAC  
 AGAGCTCGGCTGAGCCGGGTACCAGGCTGGCATCCCCCTTCTCTTCTTGGAGCTTCAGACCG  
 GGATGAGCCAGGCACAGCCAACTCGGATCTTCGATTCACATCCTGAGCCAGGCTCCAGCCAGC  
 CTCCCCAGACATGTTCCAGCTGGAGCCTCGGCTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGC  
 ACCAGCCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA  
 CCAGGCCTCAGGCCACCAGGCCACTGCCACCGTGGAACTCTCCATCATAGAGAGCACCTGGGTGT  
 CCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCTTATACCCGCACCACATGGCCAGGTA  
 CACTGGAGTGGGGGTGATGTGCACTATCACCTGGAGAGCCATCCCCGGGACCCCTTGAAGTGAA  
 TGCAGAGGGAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCC  
 AGGTGCGGGCTCAGAATTCCTCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCAGCTGCTGGT  
 ATGGATGAGAATGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCT  
 CAGTCCACCAGGTACTGAAGTGACTAGACTGTGAGCAGAGGATGCAGATGCCCCCGGCTCCCCCA  
 ATTCCACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTC  
 CAGGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACAT  
 CCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGTGAAG  
 TCGAAGTCGCAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCAGATTGGGCCT  
 ATAAGCCTCCCTGAGGATGTGGAGCCCGGACTCTGGTGGCCATGCTAACAGCCATTGATGTGA  
 CCTCGAGCCCGCTTCCGCCCTCATGGATTTTGCCATTGAGAGGGGAGACACAGAAGGGACTTTTG  
 GCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG  
 GCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCCC  
 AGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGTGATGCCACCCCCCAAGTTGG  
 ACCAGGAGAGCTACGAGGCCAGTGTCCCATCAGTGCCCCAGCCGGCTCTTCTGTGCTGACCATC  
 CAGCCCTCCGACCCCATCAGCCGAACCCCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCT  
 CTGCATTGAGAAATCTCCGGGGAGGTGCACACCGCCAGTCCCTGCAGGGCGCCAGCCTGGGG  
 ACACCTACACGGTGCTTGTGGAGGCCAGGATACAGCCCTGACTCTTGCCCTGTGCCCTCCCAA  
 TACCTCTGCACACCCCGCAAGACCATGGCTTGATCGTGAGTGACCCAGCAAGGACCCGATCT  
 GGCCAGTGGGCACGGTCCCTACAGCTTACCCTTGGTCCCAACCCACGGTGCAACGGGATTGGC  
 GCCTCCAGACTCTCAATGGTTCCCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCAGT  
 GAACACATAATCCCCGTGGTGGTGCAGCCAAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGAT  
 CGTGCTGCTGCAACGTGGAGGGGAGTGCATGCGCAAGGTGGGCCGATGAAGGGCATGCCCCA  
 CGAAGCTGTGCGCAGTGGGCATCCTTGTAGGCACCCCTGGTAGCAATAGGAATCTTCTCATCCTC  
 ATTTTACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCCCT  
 GAAGGCGACTGTCTCAATGGCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAG  
 TCCCTGGGAGAGAGCCAGCACCCAAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCTCCA  
 TCTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCACTT  
 TATGGACTGCCCATGGGAGTGCTCCAATGTGAGGGTGTGTTGCCCAATAATAAGCCCCAGAGAA  
 CTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

## FIGURE 98

MVPAWLWLLCVSVPQALPKAQAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT  
 EGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPPVLVHVKDENDQVPHFSQAI  
 YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRLGALALSPKG  
 STSLDHALERTYQLLVQVKMDQASGHQATATVEVSI IESTWVSLEPIHLAENLKVLYPHHMAQ  
 VHWSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQNSHGEDIYAAPLELHVL  
 VMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSHVYQLLSPEPEDGVEGRA  
 FQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSSTCEVEVAVTDINDHAPEFITSQIG  
 PISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTEGTFGLDWEPPDSGHVRLRLCKNLSY  
 EAAPSHEVVVVQSVAKLVGPGPGGATATVTVLVERVMPPPKLDQESYEASVPISAPAGSFLLT  
 IQSPDPISRTLRFSLVNDSEGWLCIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALTAPVPS  
 QYLCTPRQDHGLIVSGPSKDPDLASGHGFPYSFTLGPNPTVQRDWRLQTLNGSHAYLTALHWVEP  
 REHIIPVVVSHNAQMWQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTILVAIGIFLI  
 LIFTHWTMSRKKDPDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

## FIGURE 99

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACGCCTG  
 AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTA  
 TCTCTTCACCTTCAAGTCCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCTTGGTAC  
 ATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG  
 TTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCCAATGAGACTAGCACC  
 TCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCCAG  
 TGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGGGGTCA  
 GCATAGTCACCAACTCTGAGTTCCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG  
 TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGG  
 GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTCCACCAACT  
 CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC  
 AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCAC  
 AACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA  
 CCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT  
 GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG  
 AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACAGACCTCCAGTGGGGCCA  
 GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAG  
 TCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG  
 GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACT  
 CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCTCC  
 AGTGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAACACAGCCAC  
 CAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA  
 CCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACA  
 GCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAG  
 CACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCA  
 ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGA  
 ATGCACACAATTCCCATAGTGCATCTACTGCAGTGAAGTGAAGCAAGCTGGTGGGTCCCTGGT  
 GCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGGCGTGGGGCTCTTTGCTGGGC  
 TCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGTCTACCACCT  
 CATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCAGGCCAG  
 GTGGAGTCTTAAGTGTTCGGAGGAGACCAGTATCATCGATAGCCATGGAGATGAGCGGGAGGA  
 ACAGCGGGCCCTGAGCAGCCCCGAAGCAAGTGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCA  
 CCCAAGACCTGGTTTCTTTTCATTATCCAGGAGACCCCTCCAGCTTTGTTTGAGATCTGAA  
 AATCTTGAAGAAGGTATTCTCACCTTTCTTGCCTTTACCAGACACTGGAAAGAGAATACTATAT  
 TGCTCATTTAGCTAAGAAATAAATACATCTCATTAACACACAGACAAAGAGAAGCTGTGCTTG  
 CCCCCGGGTGGGTATCTAGCTCTGAGATGAATCAGTTATAGGAGAAAACCTCCATGCTGGACTC  
 CATCTGGCATTCAAAATCTCCACAGTAAAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

# **FIGURE 100**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGS  
 SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS  
 GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTSSGASTA  
 TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTNGAGTATNSES  
 STTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNSDSSTTSS  
 GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA  
 TNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESSTVSSGISTVTNSES  
 STTSSGANTATNSGSSVTSAGSGTAALTMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA  
 AVGLFAGLFFCVRNLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAPHRPRWSPNWFRRPVSSI  
 AMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532



# **FIGURE 101**

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCCTA  
CGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTACAGGTG  
GGAGGCTGGAACTATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCAACAAAT  
GGATGATGTGATATATGCAATTCCAGGGGAAGGAAATTGTGGTGCTTCTGAACCCATGGTCAATT  
AACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCTTTGGAATCAT  
GGTGTGTCATGGAAAGGATTACTTTTATACTGACTCTGTTTTGGGGAAGCTTTTTTGGGAAGCATTT  
TCATGCTGAGTCCCTTTTACCTTTTGATGTTTGTAAACCCATCTTGGTATCGCTGGATCAACAAC  
CGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCATGTTTGGTGTAAGT  
GATTATACTGGGGATGCATTTGTTCTGGAGAAAGAAGTGTATTATCATGAACCATCGGACAA  
GAATGGACTGGATGTTCTGTGGAATTGCCTGATGCGATATAGCTACCTCAGATTGGAGAAAATT  
TGCCTCAAAGCGAGTCTCAAAGGTGTTCTCGATTGTTGGTGGGCCATGCAGGCTGCTGCCTATAT  
CTTCATTATAGGAAATGGAAGGATGACAAGAGCCATTTTGAAGACATGATTGATTACTTTTGTG  
ATATTCACGAACCACTTCAACTCCTCATATTTCCAGAAGGGACTGATCTCACAGAAAACAGCAAG  
TCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTCAGAAATATGAATATGTTTTACATCCAAG  
AACTACAGGCTTTACTTTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCCTTGATGCTGTCCATG  
ATATCACTGTGGCGTATCCTCACACATTCCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT  
CCCAGGGAAATCCACTTTACGTCCACCGGTATCCAATAGACACCCTCCCAACATCCAAGGAGGA  
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAAGAAGAGAGGCTGCGTTCTTCTATCAAG  
GGGAGAAGAATTTTTATTTTACCGGACAGAGTGTCAATCCACCTTGCAAGTCTGAACTCAGGGTC  
CTTGTGGTCAAATTGCTCTCTATACTGTATTGGACCCTGTTTCAAGCCCTGCAATGTGCCTACTCAT  
ATATTTGTACAGTCTTGTAAAGTGGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGA  
GAATATTTGGTGGACTGGAGATCATAGAACTTGCATGTTACCGACTTTTACACAAACAGCCACAT  
TTAAATTCAAAGAAAAATGAGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTG  
GAAATGTTCTAAACCTTTCTAAGCTCAGATGCATTTTTCATGACTATGTCGAATATTCTTACT  
GCCATCATTATTTGTTAAAGATATTTTGCATTAATTTTGTGGGAAAAATATTGCTACAATTTTT  
TTAATCTCTGAATGTAATTTTCGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTT  
GGGCCAGAATATTATTAAACAATCATCAGGCTTTTAAA

## **FIGURE 102**

MHSRGREIVLLNPWSINEAVSSYCTYFIKQDSKSFIMVSWKGIYFILTLFWGSFFGSIFMLSP  
 FLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM  
 FLWNCLMRYSYLRLEKICLKASLKGVPFGWAMQAAAYIFIHRKWKDDKSHFEDMIDYFCDIHEP  
 LQLLIFPEGTDLTENSKSRNAFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDITVA  
 YPHNIPQSEKHLQGDFFPREIHFFVHRYPIDTLPTSKEDQLWCHKRWEEKEERLRSFYQGEKNF  
 YFTGQSVIPPCKSELRLVVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG  
 LEIIELACYRLHLHKQPHLNSKKNE

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-22

#### **Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGACC  
TCCAAATCTTCATCCACCCTGCTGTGTCATCTGTTTTCATAGTGTGAGATCAACCCACAGGAATA  
TCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTCTTACAGAGCTGGTGTACAGGACAGTGGCAAGT  
CATGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGAGGACGCCGTGTTCTCTGCTCCCTCT  
TTCCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTCTCTCAGGAATCAGTTCCATGCTGTGGTC  
CACCTGTACAGAGATGGGGAAGATCGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAACCTGA  
GTTTGTGAAGGACTCCATTGCGAGGGGGCGGTGTCTCTTAAGGATAAAAACATCACTCCCTCGG  
ACATCGGCCCTGTATGGCTGTGGTTTCAGTTCGCCAGATTACGATGAGAGGCCACCTGGGAGCTG  
CGGGTGGCAGCACTGGGCTCACTTCCCTCATTTCCATTCGTGGGATATGTTGACGGAGGTATCCA  
GTTACTCTGCCTGTCTCAGGCTGGTTCCTCCAGCCACAGCCAAGTGGAAAGGTCCACAAGGAC  
AGGATTTGTCTTCAGACTCCAGAGCAAAATGCAGATGGGTACAGCGCTGTATGTGTGGAGATCTCC  
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTTTCATCCACCTTGCTGAGCAGAGTCATGA  
GGTGGAAATCCAAGTATTGATGAGGAGAGACGTTTTTTCAGCCCTCACCTTGGCGCTGGCTTCTA  
TTTTACTCGGGTACTCTGTGGTGCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTC  
AAATCCAAAGGGGAAAAATCCAGCGGGAATCGGACTGGAGAGAAAGAACCGGACAGGCAGCAATTGAG  
AGACGCCCGGAAACAGCAGCTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCGG  
TTCTGTATCTGAAACTGTAAACCATAGAAAAGCTCCCCGAGGAGGTGCCCTCACTCTGAGAAGAGA  
TTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA  
CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGCGGGATGACGTAGACAGGGGGAAGAAC  
ATGTGACTTTGTCTCCCAACAATGGGTATTGGGTCCTCAGACTGACACAGAACATTGTATTTC  
ACGTTCAATCCCCATTTTATCAGCCTCCCCCCCCAGACCCTCTCTACAGAGTAGGGGTCTTCTCT  
GGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGC  
TGACATGTCAGTTTGAAGGCTGTGTGAGACCTATATCCAGCATGCAATGTATGACAGGAGAAAG  
GGACTCCCATATTCATATGTCAGTGTCTCTGGGATGAGAGACAGAGAACCTGCTTAAAGGGC  
CCCACACACAGACCAGACACAGCCAAGGGAGAGTGCTCCGACAGGTGGCCCCAGCTTCTCTCT  
CCGGAGCCTGCGCACAGAGAGTACGCCCCCCTCTCTCTTATAGGGAGCTGAGGTCTCTTGCCC  
TGAGCCTGTCAGAGCGCGGCGAGTCAGAGTCCAGATGAGGGGGATGGCCTGACCCTGTGGGAG  
TCAGAACCTGCATGGCTGCCCTGAAGTGGGACGGAATAGACTCACTAGGTTAGTTTGTGAAAA  
CTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCAGGCTCCTCATTGTTGCTAGTCAGG  
ACAGTGATTCCTGCCTCACAGGTGAAGATTAAGAGACAACGAATGTGAATCATGCTTGCAGGTT  
TGAGGGCAGAGCATGTTTGCTAATGATGTGTTTTATATTATACATTTCCACCATAAATCTGTT  
TGCTTATTCCACATTAATTACTTTTCTCTATACCAATACCCCATGGAATAGTTATTGAACACC  
TGCTTTGTGAGGCTAAAGAATAAAGAGAGGAGGTAGGATTTTCACTAGTTCTATAAGCCAGCAT  
TACCTGATACCAAAACCAGGCAAAGAAAAACAGAAGAAGAGGAAGGAAAACTACAGGTCCATATCC  
CTCATTAACACAGACACAAAATCTTAATAAAATTTTAAACAATTAACATAAACAAATATTTTA  
AAGATGATATATACTACTCAGTGTGGTTTGTCTCCACAAATGCAGAGTTGGTTTAAATATTTAAAT  
ATCAACCAGTGTAAATCAGCAGATTAATAAGTAAAAAAGAAAAACCTATAAAAAA

# **FIGURE 104**

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH  
 LYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR  
 VAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLYDVEISI  
 IVQENAGSILCSIHAEQSHEVESKVLIGETFFQPSWRLASILLGLLCGALCGVVMGMIIVFFK  
 SKGKIQAELDWRKKGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF  
 TRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSPNNGYWVLRLTTEHLYFT  
 FNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLCQFEGLLRPYIQHAMYDEEKG  
 TPIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

## FIGURE 105

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG  
 TTTGTTGGGAACCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTCTGGCAGTGTGCATTGGA  
 CTCACCTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAATTACTATAGCACATTGTCAATTACAAC  
 TGACAAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAAATTTACAGAAATGAGCCAGAGACTTGAAT  
 CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTC  
 AGTCAACAGAAGCATGGAGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACCTCTACTGAGGATCCTGA  
 AACTGTAGATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGACCCCCATAAGTAG  
 ATCCTCACTCAGTTAAAATTAAAAAATCAACAAGACAGAACAGACAGCTATCTAAACCATTGCTGCCGA  
 ACACGAAGAAGTAAACTCTAGGTGAGGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGAGGGTGAATG  
 GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCTCGCTGTGGAGCAACCTTAATTAATGCCACATGGC  
 TTGTGAGTGCTGCTCACTGTTTACAACATATAAGAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACA  
 ATAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACA  
 TGACTATGATATTTCTCTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTC  
 TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTGGAGCACTGAAAAAT  
 GATGGTTACAGTCAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTGCAATGAACC  
 TCAAGCTTACAATGACGCCATAACTCCTAGAAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGCAT  
 GCCAGGGTGACTCTGGAGGACCACTGGTTAGTTTACAGATGCTAGAGATATCTGGTACCTTGCTGGAATAGTG  
 AGCTGGGGAGATGAATGTGCGAAACCAACAAGCCTGGTGTATTAAGTAGAGTTACGGCCTTGCGGGACTG  
 GATTACTTCAAAAATGGTATCTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTTG  
 GGTGTGGAGGCCATTTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCA  
 ATAACTGTTTGCTTGATGCATGTATTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA  
 GATCAACTCTGTCTGTGAGCAATAGTTGAACTTTATGTACATAGAGAAATAGATAATACAATATTAC  
 ATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTGTGAGAATTTGACTTGTGACATAAATTTGTAAT  
 GCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCTCAGCTCCTCTCATTTCAGCAAATATCCATTT  
 TCAAGGTGCAGAACAGGAGTGAAGAAAATATAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAA  
 AAGTATTAGGTGTTTTCTTAGTGGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACA  
 GCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAAGTAAAGTAAAGGAAGTCCAGAAAGAAGCCAAG  
 ATATATCCTTATTTTCATTTCCAACAACACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTGTGACCT  
 ATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAAGCAAATATTTATTTAACATTG  
 TTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

DATE RECEIVED

Transmembrane domain:  
amino acids 21-40 (type II)

## FIGURE 107

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCCTG  
 CCCCAGATGAGCCCCCGCCGTGCGTCCCGGACTATCCCCAGGCGGGCGTGGGGCACCAGGGCCAGC  
 GCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTT  
 ACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGCTGCGCTGCCTGCTCTACGCCCTCAA  
 TCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAA  
 ATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTTACTTTTCT  
 GTGGTTCATCCGGTCATGATTGCTGTTGCTGTTTTCCTTATCATTGTGGGGATGTTAGGATATTG  
 TGGAACGGTGAAAAGAAATCTGTTGCTTCTTGTCATGGTACTTTGGAAGTTTGCTTGCTATTTTCT  
 GTGTAGAAGTGGCTTGTGGCGTTTGGACATATGAACAGGAAGTTATGGTTCCAGTACAATGGTCA  
 GATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCA  
 TGCTTGAATTTTTTTCAGAGAGAGTTAAGTGCTGTGGAGTAGTATATTTCACTGACTGGTTGG  
 AAATGACAGAGATGGACTGGCCCCAGATTCTGTCTGTGTAGAGAATCCCAGGATGTTCCAAA  
 CAGGCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAATGTATTTCCCT  
 TTTGAGAGGAACCAACAAGTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAA  
 TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGG  
 ACAGACCAATGATGTCTTGAAGAATGACAACCTCTCAGCACCTGTCTATGTCCTTCAGTAGAAGT  
 GTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACT  
 TTGAGATGGAGGAGTTATAAAAAGAAATGTCACAGAAGAAAACCAAACTTGTTTTATTGGACT  
 TGTGAATTTTTGAGTACATACTATGTGTTTTCAGAAATATGTAGAAATAAAAATGTGCCATAAAA  
 TAACACCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCTATAAGTC  
 ACCACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC  
 TGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCA  
 TCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAA  
 CTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA  
 CTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACCTTCAATATTGGTGACT  
 ACCTAAATGTGATTTTTGCTGGTTACTAAAAATATTCTTACCACCTTAAAAGAGCAAGCTAACACAT  
 TGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGAT  
 TTCAGTTCTGATAATGTTAAGAATAACCATATGAAAAGGAAAATTTGTCCTGTATAGCATCATT  
 ATTTTTAGCCTTTCTGTAAATAAAGCTTTACTATTCTGTCTGGGCTTATATTACACATATAAC  
 TGTATTTAAATACTTAACCACTAATTTTGAATATTACCAGTGTGATACATAGGAATCATTATTC  
 AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTACAGA  
 AAGGACTTGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTGACACTAAACACTTTTTAAAAA  
 GCTTATCTTTGCCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAA  
 TAGTGTCTTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAACATGTGACAATTTAGAGATT  
 CTTTGTTTTATTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAATTTTTTTTACAA  
 GAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTATTAT  
 TTCTCAGAATATGGAAAGAAAATTAATATGTGTCATAAATATTTTCTAGAGAGTAA

## **FIGURE 108**

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVVHP  
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT  
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGCSKQAHQ  
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREPGTDQM  
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248



## FIGURE 109

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCTCTGATAAAGCCCTTACCAGTGCT  
GATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCTTAAAAAAGTGTGAAAGAGAAGGGGACAAAGGAACA  
CCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTCCAGAAGGATGCTCCATTCTGCTTCTCACCTG  
CCTCTTCATCACAGGCACCTCCGTGTACCCCGTGGCCCTAGATCCTTGTCTGCTTACATCAGCCTGAATGAGC  
CCTGGAGGAACACTGACCACCAAGTTGGATGAGTCTCAAGGTCTCTCTATGTGACAACCATGTGAATGGGGAG  
TGGTACCCTTACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAACCCA  
CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAGGCGACGGCATTGTGCAACGCCAGGCTTGTGCCAGCT  
TCAATGGGAAGTGTGTCTCTGGAACACCACGGTGAAGTCAAGGCTTGCCTGGAGGCTACTATGTGTATCGT  
CTGACCAAGCCAGCGTCTGCTTCCACGTCTACTGTGGTCATTTTTATGACATCTGCGACGAGGACTGCCATGG  
CAGCTGCTCAGATACCAGCGAGTGCACATGCGCTCCAGGAAGTGTGCTAGGCCCTGACAGGCAGACATGCTTTG  
ATGAAAATGAATGTGAGCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCTACCGTGT  
GAGTGTGGGGTTGGCCGTGTGCTAAGAAGTGTGCAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA  
TGGTGGCTGCAGCCACTCTGCGCTTGGATCTGAGAAAGGCTACCAGTGTGAATGTCCCCGGGGCTGGTGTGT  
CTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAAATCAAATGCCATTGAAGTGAACATCCCCAGGGAG  
CTGGTTGGTGGCCTGGAGCTCTTCTGACCAACACCTCTGCGGAGGAGTGTCAACGGCACCCATGTCAACAT  
CCTCTTCTCTCAAGACATGTGGTACAGTGGTGTGATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGA  
CAGGTCTACCAAGCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACAGCAAGTGTGATCCCGGTG  
ACCTGCGAGTTTCCACGCCTGTACACCATTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCCACTGGAAAT  
CATGAGCCGAAATCATGGGATCTTCCATTCACTCTGGAGATCTTCAAGGACAATGAGTTGAAGAGCCTTACC  
GGGAAGCTCTGCCCACCTCAAGCTTCGTGACTCCCTCTACTTTGGCATTGAGCCCCTGGTGCACGTGAGCGGC  
TTGGAAAGCTTGGTGGAGAGCTGCTTTGCCACCCCACTCCAAGATCGACGAGGTCTGAAATACTACCTCAT  
CCGGGATGGCTGTGTTTCAAGTGTGAGTACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGG  
TCCCTGTCTTCAAGTTTGTGGGCAAAGACCACAAGGAAGTGTCTGCACTGCCGGGTCTTGTCTGTGGAGTG  
TTGGACGAGCGTTCCCGCTGTGCCCAGGGTTGCCACCGCGAATGCGTGTGGGCAGGAGGAGGACTCAGC  
CGGTCTACAGGGCCAGACGCTAACAGCGGCCCGATCCGCATCGACTGGGAGGACTAGTTCGTAGCCATACCTC  
GAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTCCCCCACCAGCCCTTAAGAACATCTGCCAACAGC  
TGGGTTTCAAGTTCACACTGTGAGTTCAGACTCCCAGCACCAACTCACTCTGATTCTGGTCCATTAGTGGGCA  
CAGGTACAGCACTGCTGAACAATGTGGCCTGGGTGGGTTTCTCTTAGGGTTGAAAACCTAACTGTCCA  
CCCAGAAAGACACTCACCCATTCCCTCATTTCTTCTTACACTTAAATACCTCGTGTATGGTGAATCAGAC  
CACAAAATCAGAAGCTGGGTATAATATTCAAGTTACAAACCCTAGAAAAATTAACAGTTACTGAAATTATGA  
CTTAAATACCAATGACTCCTTAAATATGTAATTTATAGTTATACCTTGAATTTCAATTCAAATGCAGACTAA  
TTATAGGAATTGGAAAGTGTATCAATAAACAGTATATAATTTT

## FIGURE 110

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHLQDESQGPPLCDNHVNGEWYHFTGMAGDAMP  
TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYIYVRLTKPSVCFHV  
YCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV  
LRSDGKTCEDEVEGCHNNNGGCSHSLGSEKGYQCECPRGLVLSNHTCQVPVLCKSNAIEVNIIPRELVGG  
LELFLTNTSCRGVSNNGTHVNIILFSLKTCGTVVDVVDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT  
CEFRLYTISEGYVPNLRNSPLEIMSRNHGIFFTLEIFKDNEFEFPYREALPTLKLRLDSLYFGIEPVVHV  
SGLESLVESCFAFPTSKIDEVLKYLLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV  
LVCGVLDESRCAQGGCHRRMRRGAGGEDSAGLQGQTLTGGPIRIDWED

### Important features of the protein:

#### Signal peptide:

amino acids 1-16

#### N-glycosylation sites.

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

#### Tyrosine kinase phosphorylation sites.

amino acids 411-418, 443-451

#### N-myristoylation sites.

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
522-528, 531-537

#### Aspartic acid and asparagine hydroxylation site.

amino acids 197-209

#### ZP domain proteins.

amino acids 431-457

#### Calcium-binding EGF-like proteins.

amino acids 191-212, 232-253

# **FIGURE 111**

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG  
 GCCTCCTCCAGCCAGTGTCTGACCAGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCT  
 CCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT  
 TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCCGAAACCCCGTATCCCC  
 ATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTTGT  
 GGTGTCTCATCAAGGTGATTCTGGATAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCCCGA  
 GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC  
 CCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC  
 AGGGAACGTGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG  
 GCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGATGTGTTGAAATCACAGAAAACAGCCAG  
 GAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTG  
 TGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGGAGGAGCCCTCTGTGGATTCTTGGCCTTGGCAGG  
 TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCTTGACCCCCACTGGGTCTCACGGCA  
 GCCCCTGCTTCAGGAAACATACCGATGTGTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAG  
 CTTCCTATCCCTGGCTGTGGCCAAGATCATCATCATTTGAATTCAACCCCATGTACCCCAAGACAATGACA  
 TCGCCCTCATGAAGCTGCAGTTCCTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT  
 GATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTTGGATGGGGCTTACGAAGCAGAATGGAGGGA  
 GATGTCTGACATACTGTGTCAGGCGTCAGTCCAGGTCAATGACAGCACACGGTGCAATGCAGACGATGCGT  
 ACCAGGGGGAAGTCACCGAGAAGATGATGTGTGTCAGGCATCCCGAAGGGGGTGTGGACACCTGCCAGGGT  
 GACAGTGGTGGGCCCCGTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG  
 CTGCGGGGGCCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT  
 GGAAGGCTGAGCTGTAATGCTGCTGCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCTGCTGCCCTGCCACCT  
 GGGGATCCCCCAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTGCCCACAGCCTCAGCAT  
 TTCTTGGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGCCCTCGCAGCCCAGAGGCGCCAGAGGAAGTCA  
 GCAGCCCTAGCTCGGCCACACTTGGTGCTCCCAGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCT  
 CAGGGGTATTGCTAAGCCAAGAAGGAACCTTTCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAAAGCC  
 CAGATCACTGTGGCTGGAGAGGAGAAGGAAAGGCTGTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAA  
 GCCTACTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT  
 ACTGTTGTATTGTTATACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAA  
 AAAA

[illegible]

Transmembrane domain:  
amino acids 32-53 (typeII)

# **FIGURE 113**

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGATTA  
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTCAGCAACTAAAAAGCCACAGGAGT  
TGAAGTGTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAAAATC  
TGTTTTTTGTTCTCTTGTAAGTACCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT  
GGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCTCGAAG  
CCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAACTGTCTCACGTCT  
GGAGGCACTGACTCGGGCAGTGAGGTAGCTGAGCCTCTTGGTAGCTGCGGCTTCAAGGTGGGC  
CTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTTATAGGCGATGGTCCCACTGCC  
AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGGGCCGTGGACACCTGTCTA  
GAAGCAGTGGGTGAGACATCACGCTGCCCGCCATCTAACCTTTTCATGTCTGCACATCACCTG  
ATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC  
CAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGACTTGCATTCTCTGGAACATGAGG  
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACTTGTGCCAAATTATGGGTGAGAAAAGATG  
GAGGTGTTGGGTATCACAAAGGCATCGAGTCTCTGCATTAGTGAGCATGTGGGGGAAGGGCTG  
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGAT  
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA  
TCTGCGATCACCAGCCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCTCCC  
CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG  
GGCTAATGGCTCAGTGTTGGCCCAGGAGGTGAGCAAGGCCCTGAGAGCTGATCAGAAGGGCCTGCT  
GTGCGAACACGGAAATGCCCTCCAGTAAGCACAGGCTGCAAAATCCCAGGCAAAGGACTGTGTGG  
CTCAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCAAGACCAAAGGAGCTAGAGCTTGTTT  
CAAATGATCTCCAAGGGCCCTTATACCCCAGGAGACTTTGATTTGAATTTGAAACCCCAATCCA  
AACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACAT  
TTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGG  
TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATC  
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA  
GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAGAATTA  
TGGTTATTTGTAA

### **FIGURE 114**

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC  
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

**Signal peptide:**  
amino acids 1-15







## FIGURE 117

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCGGCA  
GGGCGGGCGGCCAGGATCATGTCCACCACCACATGCCAAGTGGTGGCGTTCTCCTGTCCATCCTGGGGCT  
GGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGGACCTGTACGACAACCCCGTCACCT  
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCC  
TATTTCACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCT  
GGGTGCCATTGGCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG  
CCAAAGCCAAACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTG  
TCTGTGTTTGCCAACATGCTGGTGACTAATTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGG  
GATGGTGCAGACTGTTTCAGACCAGGTACACATTTGGTGGCGCTCTGTTCTGTTGGGCTGGGTGGCTGGAGGCC  
TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAGAAGAAACCACTACAAA  
GCCGTTTCTTATCATGCCTCAGGCCACAGTGTTCCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTT  
TGGGTCCAACACCAAAAACAAGAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC  
CTTCCAAGCAGCACTATGTGTAAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGTCA  
CCCAAAAAACAAGGAGATCCCATCTAGATTTCTTCTTCTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCT  
CGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACA  
GCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTCTTTTTTAAATATAACT  
TTCTACTCTGATGAGAGAATGTGGTTTAATCTCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTC  
TTCCCTCCTAGTCAATAAAACCAATTGATGATCTATTTCCAGCTTATCCCCAAGAAAACCTTTGAAAGGAAA  
GAGTAGACCCAAAGATGTTATTTTCTGTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAA  
ACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTCTCT  
ACACTGTGATCTTAAAAGTTACCAAACCAAGTCATTTTCAGTTTGAGGCAACCAACCTTCTACTGCTG  
TTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGAGTCTCTTCTGT  
CGCGGGTCAGAAATGTCCCTAGATGAATGAGAAAATATTTTTTTTAATTTAAGTCCTAAATATAGTTAA  
AATAAATAATGTTTATGTAATGATACACTATCTCTGTGAAATAGCCTCACCCTACATGTGGATAGAAG  
GAAATGAAAAATAATGTCTTTGACATGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTC  
ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCGAGAAGT  
TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCA  
TGGTGGCATAACCTGTAGTCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCAGGGAGGT  
TGGGGCTGCAGTGAGCCATGATCACACCCTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA  
AATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATTCTTTAA

## **FIGURE 118**

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVVFQYEGLRSCVRQSSGFTECRP  
YFTILGLPAMLOAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFIVSGL  
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA  
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDY  
V

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

## FIGURE 119

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGGAGTCC  
 AGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTG  
 GTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGAGTGTGGCCTTCATT  
 GAAAACAACATCGTGGTTTTTGAAAACTTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA  
 CATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTCTCCGGACCTACAGGCAGCCAGAG  
 GACTGATGTGTGCTGCTTCCGTGATGTCCTTCTTGGCTTTCATGATGGCCATCCTTGGCATGAAATGC  
 ACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT  
 CATCACGGGCATGTTGGTGTCTATCCCTGTGAGCTGGGTGGCCATGCCATCATCAGAGATTTCTATA  
 ACTCAATAGTGAATGTTGCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCA  
 CTGGTGTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTTGTGCAACGAAAAGAGCAGTAGCTA  
 CAGATACTCGATACCTTCCCATCGCACACCCAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCG  
 TCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAATG  
 ACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAGAACTTTGATTACTGTTCTTAACTGCCT  
 AATCTTAATTACAGGAAGTGTGCATCAGCTATTATGATTCTATAAGCTATTTTACGAGAATGAGATA  
 TTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTA  
 CTCTTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAATTTCTCC  
 ACGACATAGCATTATGTACATAGATGAGTGTAACTTTATATCTCACATAGAGACATGCTTATATGGT  
 TTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAA  
 ATCATGGATAGGGTTGAAGAAGGTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCA  
 TTTATAATGAAGATTTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATAT  
 GCTGTTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCCAGAGGCTTTTTTTTT  
 CTTGTGTATTAAATTAACATTTTTTAAACGCAGATATTTTGTCAAGGGGCTTTCATTCAAAGTCTT  
 TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTG  
 AAAATATTTTTGTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGAT  
 ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAAATA  
 TGTCTTGGTTTTTCATTGCTTACCAAAAAACAACAACAAAAAAGTTGTCTTTGAGAACTTCACCT  
 GCTCCTATGTGGGTACCTGAGTCAAAATGTGATTTTGTCTGTGAAAAATAAATTTCTTCTTGTA  
 CCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTCTGTTTATCCAAATTTGATGAA  
 ACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTT  
 TATACATTTATATTAATAAATGTACATTTTCTAATT





## **FIGURE 122**

MRPQGPAA SPQRLRGLLLLLLLQLPAPSSASEIPK GKQKAQLRQREVVDLYNGMCLQGPAGVPGR  
DGS PGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDL GKIAECTFTK  
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAEC SGPLPIEAI IYLDQGSPEMNSTINIHR TS  
SVEGLCEGIGAGLVDVAIWVGTCSDYPKG DASTGWNSVSRIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

**FIGURE 123**

CTGTAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCGAGCTCTGTGGCTGAA  
CTGGGTGCTCATCAGCGGAATCTGTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA  
ATTGCTTGGGAAGAATACATCATCTTTTCGATAAGAAGAATTTGAGGATCCAGTTTTTTTTTTA  
ACGCCCCCTCCCCACCCCCCAAAAAAATGTAAGATGCAAAAACGTAATATCATCAAGATCC  
TATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTTGTTCTTGGAG  
TGTTCTGCTGGTGGCTGCGAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAGGGGTCCAAATTTT  
TCTTCTGGGTGTGACGCGCCCTGACTCACTACAGTCAGCTGACAGGGGCTGTCTGCAACT  
GCCCTTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAACAATACAAAAGTATGGGTTTCAATG  
TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCACTGTCTTACTGACAATG  
CTTTCTTCTGCCGACAGGAGTACCTTAAGGGCTGTAGGTGTGAAGGCCAAAATGGTATATTGTGA  
ATCTCAGAAATACAGGAGATACCTTCAAGTATATCTGCTGGTTGCTTAGGTTGCTCCCTTCGCT  
ATAACAGCCTTCAAAAATTAAGTATATCAATTTAAAGGCTCAACGAGTCACTCGGTATATAC  
CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTTAATGGAATACGCAGACTCAAAGA  
GCTGATTCTTAGTTCCAATAGAATCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAAT  
TAGGAACTTGTGATCTGTGCTATAATCAGTGCATTTCTCTGGGATCTGAACAGTTTTCGGGGCTTG  
CGAAGCTTCTGAGTTTACAATTTACGGTTCAACTCCCTGAGAACCATCCCTGTGCGAATTTCCA  
AGACTGCGCAACCTGGAACCTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATG  
TCTTTGCTGGCATGATCAGACTCAAAGAATTTCACTGGAGCACAATCAATTTTCCAAGCTCAAC  
CTGGCCCTTTCCTCAAGGTTGGTCAGCCTTCAGAACCCTTACTTGCAGTGAATAAAATCAGTGT  
CATAGGATGACCAATGTCTTGAGCTGGAGTCTCTACAAAGGCTTGATTTATCAGGCAATGAGA  
TCGAAGCTTTTCAAGTGGACCGCATGTTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGAT  
TCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGATATCCCTCAATGACATCAG  
TCTTGGTGGGAATATATGGGAATGCAGCAGAAATTTTGTCTCCCTTGTAACCTGGCTGAAAAGTT  
TTAAAGCTTCAAGGAGAAATACAATATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTG  
ATCGATGCAAGTGAAGAAGTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAG  
GGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCGAGGCCGAAGCATGAGAGCAAACCCCTT  
TGCCCCGACGTTGGGAGCCACAGAGCCCGCCGAGAGCCGATGCTGACGCCGAGCAGCATCTCT  
TTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTCTCGTCACTCTGCTGATTTAT  
CTACGTGTCATGGAAGCGGTACCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGTGCGAA  
GGCAGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCCAGCACCCAGGAATTTTATGTA  
GATTATAAACCCACCAACAGGAGACAGCGAGATGCTGCTGAATGGGACGGGACCTTGACCTTA  
TAACAAATCGGGCTCCAGGGAGTGAGGATATGAACCATTTGTGATAAAAGAGCTCTTAAAGCT  
GGGAAATAGTGGTGCTTTTATGAACTCTGGTGACTATCAAGGAAACGCGATGCCCCCTCCCT  
TTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCTTGTCCGTTTTAGTGCATTATAATACT  
GCTCATTTTCTCTCATACATTAATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTT  
GAATCCGGGTTTTAATAATAAATCTATTGTATAAGACCCCTTTACTGATTCCATTAATGTCGCATTT  
GTTTAAAGATAAACTCTTTTCATAGGTAAAAA





## FIGURE 125

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCGCTG  
 ACCCAGAGATGGCCCCGAGCGAGCAAATTCTACTGTCCGGCTGCGCGGCTACCGTGGCCGAGCT  
 AGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAGCTCTTGCTC  
 GGTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC  
 ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT  
 GTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAAG  
 ATGAGCATTATCCCTTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCCAGTTT  
 TTAGCCAATCCAACCTGACCTAGTGAAGGTTGAGATGCAAATGGAAGGAAAAAGGAACTGGAAGG  
 AAAACCATTGCGATTTCTGTGGTGTACATCATGCATTTGCAAAAATCTTAGCTGAAGGAGGAATAC  
 GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTA  
 ACCACTTATGATACAGTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGAC  
 TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA  
 TCAAAAGCAGAATAATGAATCAACCACGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCG  
 ACTGACTGCTTGATTGAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACC  
 ATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAATCAGAGAGA  
 TGAGTGGAGTCAGTCCATTTTAA

## **FIGURE 126**

MSVPEEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGARES  
APYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEHYPLWKS  
VIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFKILAEGGIRGLWAGWVP  
NIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTPADVIKSRIMNQP  
RDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248



## **FIGURE 128**

MARPGMERWRDRLALVTGASGGIGAARALVQQGLKVVGCVARTVGNIEELAAECKSAGYPGTLI  
PYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPDITLLSGSTSGWKDMFNVNVLALSICTR  
EAYQSMKERNVDDGHIININMSGHRVPLSVTHFYATKYAVTALTEGLRQELREAQTHIRATC  
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-17

#### **N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

#### **Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114

## FIGURE 129

AACTTCTACATGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACCAT  
CATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTGAGGTGCAGAGTCTCAGTTGCCCGGGAGC  
ACCTCCCTCCCAGGCAGTCTGCTCAGAGGGCCTCGGCCAGAATCCAGTTCTGGTTTCATGC  
CAGCCTGTAAAGGCCATGGAACCTTGGGTGAATCACCGATGCCATTTAAGAGGGTTTCTGCCA  
GGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTCAATTCAGTAGCCACCAGCCACCTGTGG  
CCGTTGAGTGCTTGAAATTGAGGAAGTGAAGAAATTAATTTCTCATGTATTTTCTCATTTATTTA  
TTAATTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA  
TATATAATGATCAAATCAGGGTAACGGGATATCCATCACATCAAACATTTATTTTTTATTCTTT  
TTAGACAGAGTCTCACTCTGTCAACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC  
CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCCTCCACCTCCCAAGTAGCTGGGACTACAGGCAT  
GCACCACAATGCCCAACTAATTTTTGTATTTTGTAGTAGAGACGGGGTTTTGCCATGTGCCCAGG  
CTGGCCTTGAACTCCTGGCCTCAAACAATCCACTTGCCCTCGGCCTCCCAAAGTGTATGATTACA  
GGCGTGAGCCACCGTGCCCTGGCCTAAACATTTATCTTTCTTTGTGTTGGGAACTTTGAAATTAT  
ACAATGAATTATGTTAACTGTCTATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT  
ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCC  
AACCTCTGATCACCTCATTCTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCCATGTG  
AGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTG  
TTCCATCCATGTTGCTGCAAATGACAGGATTTCTGTTCTTAATTTCAATTAAAATAACACACATG  
GCAAAAA

### **FIGURE 130**

MGLLLLVLFLLPVAITIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQPV  
KGHGTLGESPMFPKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 86-92

**Zinc carboxypeptidases, zinc-binding region 2 signature.**

amino acids 68-79

**FIGURE 131**

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC  
 ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCCTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG  
 TCCATCTGTGTGTCGCTGCGATGCGGGTTTCATTTACTGTAATGATCGCTTCTGACATCCATTCCAACAG  
 GAATACCAGAGGATGCTACAACCTCTACCTTCAGAACAACCAAATAAATAATGCTGGGATTCTTCAGAT  
 TTGAAAACTTGCTGAAAGTAGAAGAATATACCTTATACCACAACAGTTTAGATGAATTTCTACCAACCT  
 CCCAAAGTATGTAAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAA  
 AAATTCCTATCTGGAAGAATTACATTTAGATGACAACCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA  
 TTCCGAGACAGCAACTATCTCCGACTGCTTTCTGTCCCGTAATCACCTTAGCACAAATTCCTGGGGTTT  
 GCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCATCTCTTCAAG  
 GTCTCACTAGTCTAAAACGCCTGGTTCTAGATGGAACCTGTTGAACAATCATGGTTTAGGTGACAAAGTT  
 TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATTCCTGACTGCTGCACCAGTAAACCT  
 TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTGCCCCAAATGCTTTTT  
 CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTT  
 GATGATTTGGACAAATAACACAACCTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATG  
 GGTACGTGACTGGTTACAATCACTACCTGTGAAGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAA  
 AGGTTCTGGGATGGCTATTAAGGATCTCAATGCAGAAGTGTGATTGTAAGGACAGTGGGATTGTAAGC  
 ACCATTCAAGATAACCACTGCAATACCCAACACAGTGATCCTGCCAAGGACAGTGGCCAGCTCCAGTGAC  
 CAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAGGGAGTCCCTCAAGAAAAA  
 CAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTTCATATCTCTTGGAACCTTGCTCTACCTATG  
 ACTGCTTTGAGACTCAGCTGGCTTAACTGGGCCATAGCCCGGCATTGGGATCTATAACAGAAACAATTGT  
 AACAGGGGAACGCAGTGAGTACTTGGTCACAGCCCTGGAGCCTGATTACCCCTATAAAGTATGCATGGTTC  
 CCATGGAAACCAGCAACCTCTACCTATTTGATGAAACTCCTGTTTGTATTGAGACTGAAACTGCACCCCTT  
 CGAATGTACAACCTTACAACCACCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACC  
 TTTGGCTGCCATCATTTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTGGTATG  
 TTCATAGGAATGGATCGCTCTTCTCAAGGAAGTGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT  
 GCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAATCAGGGAACTTCTTTTTCAGATGTTACCAAT  
 AAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAAATACACCATATTTCCCTCCTAATGGAATGAATCTGT  
 ACAAAAACAATCACAGTGAAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC  
 TCACACTCATATGATGCTGAAGGACTCACAGCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATG  
 GT

## **FIGURE 132**

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTLYL  
 QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNI RTITYDSLSKIPYL  
 EELHLLDDNSVSAVSIIEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL  
 QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQDNHIN  
 RVPPNAFSYLRQLYRLDMSNNNLSNLPQGIFDDLDNITQLILRNNPWYCGCKMKWVRDWLQSLPV  
 KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQGQWPAPVTKQPD  
 IKNPKLTKDQQTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWLKLGHSPAFGSITET  
 IVTGERSEYLVTALEPDSPYKVCMPMETSNNLYLFEDETPVCIE TETAPLRMYNPTTTLNREQEKE  
 PYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS  
 ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLKNNHSESSSNRSYRDSGIPDSHSHS

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 531-552

#### **N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

#### **Tyrosine kinase phosphorylation site.**

amino acids 515-522

#### **N-myristoylation sites.**

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,  
 640-645

#### **Amidation site.**

amino acids 567-570

#### **Leucine zipper pattern.**

amino acids 159-180

#### **Phospholipase A2 aspartic acid active site.**

amino acids 34-44



**FIGURE 133**

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCAGGCCACCCAGGCTTCTTGGA  
 GCCCTGCCGGGCCACTTGTCTTCAATGTCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG  
 TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGAGCAGAG  
 GCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACCGCTGTGGT  
 CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT  
 GCGCTGGAGAGAGCCACCGTCTTCCCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT  
 GGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCGGGGAGAAGTGGGCCCAGGAGCCCCCTGC  
 TGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC  
 CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCAGCTGACCTCCAGCCCCG  
 GTTTTGGAAAGCTCCCACATGCCTGGATCCACACTGATGCCTCCTTGGTGTACCCACGTTTCGGGC  
 CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGGACG  
 GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCGGCTGCTC  
 AGGCTACTGCCTGTCCCACCAACTGCTCTTCTCCTCTGGGCCAGAATGAGGGGATGCACACAGG  
 GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC  
 AGAGCTGAGGCCATCGGATACGCCTACCCTACCCGGGACATCTTCATGGAAAACATCATGTTCTG  
 TGAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA  
 AACAGCAGGAAGGATGCTTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA  
 TATCAGCAGCATTTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGT  
 TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGC  
 AATTCTCTTGCCCTCATCCTCCCGAGTAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAAT  
 TTTTATATTTTTTTAGTAGAGACAGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT  
 CTAAGAGATCCGCCCACCTCAGGCTCCCAAAGTGTTGGGATTATAGGTGTGAGCCACCGTGTCTG  
 GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTC  
 ATGGGGGCTCTCTCCCTAGATGGCTGCTCCTCCACAACACAGCCACAGCAGTGGCAGCCCTGG  
 GTGGCTTCTTATACATCCTGGCAGAATACCCCCAGCAAACAGAGAGCCACACCCATCCACACCG  
 CCACCACCAAGCAGCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCC  
 TTTAGTCCTCATCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG  
 ATAAGCAAAGCCACCCCGACACCCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG  
 GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAA





## **FIGURE 136**

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGSGVGIGDRFKIEGRAVVPGVKPDWISAA  
 RVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSFAYRFDVPVRVDITSKGKMRARYVNYIKTSE  
 VVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLI FVLLPKVVNTSDPDMRREME  
 QSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

**Important features of the protein:**

**Signal sequence:**

amino acids 1-23

**Transmembrane domain:**

amino acids 161-182

**N-glycosylation site.**

amino acids 184-187

**Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

**N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

**Amidation site.**

amino acids 238-241

**ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236





# **FIGURE 139**

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCAGCC  
TAGCGTGTCCACGATCGCGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCGAGGTGC  
TAGGGATCGCGGTCTTCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCCCTGTCAGAGCGGAA  
CACGGAGCGGAGCCCCAGCGCCCCGAACCTCGGCTGGAGCCAGTTCTAACTGGACCACGCTGCC  
ACCACCTCTCTCAGTAAAGTTGTTATTGTTCTGATAGATGCCCTTGAGAGATGATTTTGTGTTTG  
GGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTTACCTTGTGGAAAAAGGAGCATCTCACAGT  
TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAATCAAGGCATTGATGACGGGGAG  
CCTTCCTGGCTTTGTGACGTCATCAGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGA  
TAAGACAAGCAAAGCAGCTGGAAAAAGAATAGTCTTTTATGGAGATGAAACCTGGGTAAATTA  
TTCCCAAAGCATTTTGTGGAATATGATGGAACAACCTCATTTCGTGTGAGATTACACAGAGGT  
GGATAATAATGTCACGAGGCATTGGATAAAGTATTAAGAGAGGAGATTGGGACATATTAATCC  
TCCACTACCTGGGGCTGGACCACATTGGCCACATTCAGGGCCCCACAGCCCCCTGATTGGGCGAG  
AAGCTGAGCGAGATGGACAGCGTGCTGATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGA  
GACGCCTTTACCCAATTTGCTGGTTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACG  
GGGCCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAAATCAGTTCTGCGTTTGAAAGGAAA  
CCCGGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTGGCTGCGACACTGGCGATAGC  
ACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCAGTTTGTGAAGGAAGAC  
CAATGAGAGAGCAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAACTGTTGCAAGAG  
AATGTGCCGTCATATGAAAAGATCCTGGGTTTGAGCAGTTTAAATGTGAGAAAGATTGCATGG  
GAACTGGATCAGACTGTACTTGGAGGAAAAGCATTGAGAGTCCCTATTCAACCTGGGCTCCAAGG  
TTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCAG  
TTCTCACCTGCTCCTGCTCAGCGTCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCA  
CTGTCTATCCTGGGTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTTCGGCCGTTACGCT  
CATTGTGTGCACCTCAGCTGAAAGTTGCTGCTACTTCTGTGGCTCTCGTGGCTGGCGGCAGGCT  
GCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGTGGCAGTGCCCTGGAC  
AGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTGTCCCGACACAGGTG  
TTCACATCTGTGCTGTGAGGTGAGTGCCTCAGTTCTTGGAAAGCTAGGTTCTGCGACTGTTAC  
CAAGGTGATTGTAAAGAGCTGGCGGTCACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGTGAA  
TCGGACAGCCTCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAAGAGACAATCGGCCTGGA  
CACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCACTCATCCTGCCACCCCCAGAATGCATCCT  
GCCTCATCAGGTCCAGATTCTTTCCAAAGGCGGACGTTTCTGTTGGAATTCTTAGTCCTTGGCC  
TCGGACACCTTCATTTCGTTAGCTGGGGAGTGGTGGTGAGGCAGTGAAGAAGAGCGGATGGTCAC  
ACTCAGATCCACAGAGCCCAGGATCAAGGGACCACTGCAGTGGCAGCAGGACTGTTGGGCCCCC  
ACCCCAACCTGCACAGCCCTCATCCCTCTTGGCTTGAGCCGTGAGAGGCCCTGTGCTGAGTGT  
CTGACCGAGACACTCACAGCTTTGTATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTG  
CCACGCTTGACCTCGGGCCCATCTGGGCTCATGCTCTCTCTCTGCTATTGAATTAGTACCTAG  
CTGCACACAGTATGTAGTTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

## FIGURE 140

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGAEPPAPEPSAGASSNWTTLPPPLF  
SKVVIVLIDALRDDVFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF  
VDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTSFFVSDYTEVDNNV  
TRHLDKVLKRGDWDILILHYLGLDGHIGHISGPN SPLIGQKLSEMDSVLMKIHTSLQSKERETPLP  
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

### Important features of the protein:

#### Signal peptide:

amino acids 1-34

#### Transmembrane domain:

amino acids 58-76

#### N-glycosylation sites.

amino acids 56-60, 194-198

#### N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

#### Amidation site.

amino acids 154-158

#### Cell attachment sequence.

amino acids 205-208



# **FIGURE 141**

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACA  
GAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGTTGGAGTACAAC  
TCCCTATAGAAAACAACAGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC  
CCGAAGAAATTCAGCATTATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT  
AGCAGTTCCAGATAAAAACTACATACGCCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT  
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTAAAGGGGAGTTTGTCTCTAC  
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCT  
GGCTGCCCCAAAAGGAATCAGCACGCCGGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGA  
ACATGCTGGAGTCGGCGGCTCACCCCGGATGGTTTCATCTGCACCTCCTGCAATTGTAATGAGCCT  
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTTCAACCAGTTTGCAA  
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAACTGCCCCATTGAACGCCCTCCTCGCTA  
ATTTGAACTAATTGTATAAAAAACACCAAACCTGCTCACT

# **FIGURE 142**

MLLLLLEYNFPIENNCQHLKTTHTFRVKNLNPKKFSIHDQDHKVLVLDSGNLIAVDPKNIYIRPEI  
 FFALASSLSSASAEGKSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFI  
 FYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 33-36

**N-myristoylation site.**

amino acids 50-55, 87-92

**Interleukin-1**

amino acids 37-182

# **FIGURE 143**

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTTAA  
TCCAGGATCCTGTCCTTCCTGTCCTGTAGGAGTGCCCTGTTGCCAGTGTGGGGTGAGACAAGTTTG  
TCCCACAGGGCTGTCTGAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACCTCCTGTGGG  
CACGGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATGCTGGGCCTGCCGTGG  
AAGGGAGGTCTGTCTGGGCGCTGCTGCTGCTTCTCTTAGGCTCCCAGATCCTGCTGATCTATGC  
CTGGCATTTCACAGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA  
CAGTGGAGTTTGCTGTCCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG  
CACATCTTGAATTCTTGGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT  
GGGGAGAACTAGGTGTGGGAAATTTGAAGACGACATTGACAACCTGCCATTTCCAAGAAAGCACAG  
AGCTGAACAATACTTTACCTGCTTCTTCACCATCAGCACCAGGCCCTGGATGACTCAGTTCAGC  
CTCCTGAACAAGACCTGCTTGGAGGGATTCCACTTGAGTGAAACCCACTCACAGGCTTGTCATGT  
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTTCAGTGGCTGAGCAGCT  
TTGGACTTGTTTGTATCCTATTTTGCATGTGTTTGAGATCTCAGATCAGTGTTTAGAAAATCC  
ACACATCTTGAGCCTAATCATGTAGTGTAGATCATTAAACATCAGCATTTTAAGAAAAAAAAAAAA  
AA

## **FIGURE 144**

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY  
YAYRLGHIILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP  
WMTQFSLLNKTCLEGFH

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-25

#### **N-glycosylation sites.**

amino acids 117-121, 139-143

#### **N-myristoylation site.**

amino acids 9-15

# **FIGURE 145**

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGAAG  
CACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGGTCCA  
GACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCAGCACTGCCCAGATCA  
CTGAGGGCCAGGTGGCTGAGAACCGCCCGGGAGCCTTCATCAAGCAAGGCCGCAAGCTCGACATT  
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA  
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCTGCATCAATGCCA  
CCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG  
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGGAGAGGGGCGCAGGACT  
TCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAAT  
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT  
CTTCTCCCCCAAACCCACGCGTGTTCTGAAGGTGCCCAGGAGCGGCGATGCACTCGCACTGCAAA  
TGCCGCTCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGGACTGTGGCTTCT  
CCGTCACTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT  
GAGAAGAACACATCAGGCACTGCGCCACCTGCTTCACAGTACTTCCCAACAACCTCTTAGAGGTAG  
GTGTATTCCCGTTTTACAGATAAGGAAACTGAGGCCCAGAGAGCTGAAGTACTGCACCCAGCATC  
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCTGGCTTGCTTAACCCAGGTTTTCTGCTCT  
GTCCAATTCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCCAAACATGTAT  
CTCTAATGAAATTGTGAAAGCTCCATGTTTAGAAATAAATGAAAACACCTGA

## **FIGURE 146**

MRKHLSWWLATVCMLLFSHLSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK  
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNKLHQQ  
VLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWLMVK

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 157-171

#### **N-glycosylation sites.**

amino acids 98-102, 110-114

#### **Tyrosine kinase phosphorylation site.**

amino acids 76-83

#### **N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

#### **Amidation site.**

amino acids 62-66

# **FIGURE 147**

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCATT  
 CCTGATGATTTATAGACTCAAAGAAAACTCATGTTCAGAAGCTCTCTTCTCTTCTGGCCTCCTCT  
 CTGTCTTCTTTCCCTCTTTCTTCTTATTTAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG  
 AAATCTTTCATTTTGCTTGTGTCAGTGGGGTAGGTCAGTCTTAGTTTTTATTTTTTGAATTT  
 CAACTTTCAGATTCAGGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCATTGATGCTGAGG  
 TTTGGGGT

## **FIGURE 148**

MFRSSLLFWPPLCLLSLFLILISSIYSECKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE  
GLFYEYIA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-myristoylation site.**

amino acids 62-68



**FIGURE 149**

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCTCTACCTGGAGACTTGAC  
 TCCCGCGCGCCCCAACCTTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGCCGCCAGTCC  
 CGGCCCCCTCTCCCGCCCCACCCACCTCCTGGCTCTTCCTGTTTTTACTCCTCCTTTTCATTTCATA  
 ACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCAAGCCGAGCGTGGAAGAATGGGGTT  
 CCTCGGGACCGGCACTTGGATTCTGGTGTAGTGTCCCGATTCAAGCTTTCCCAAACCTGGAGGAA  
 GCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAA  
 GCAGAAGAAGACAAGATTAAAAAACATATCCTCCAGAAAACAAGCCAGGTGAGAGCAACTATTCTTT  
 TGTGTATAACTTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTA  
 TAAGAAGCTCCCACTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTG  
 ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCA  
 TCAACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTATGAAG  
 AAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGC  
 CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCCAACAA  
 TTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG  
 TGAATCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACAGTATCTAACACA  
 TTAACCTTGACAAATGGCTTGGAAGGAGAACTAAAACCTACAGTGAAGACAACTTTGAGGAACCTCA  
 ATATTTCCAAATTTCTATGCGCTACTGAAAAGTATTGATTGAGAAAAGAGCAAAAGAGAAAGAAA  
 CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACATATCT  
 CCAGAAGAAGGTGTTTCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCT  
 AGAAAAAATGCTACTGACAATATAAGCAAGCTTTTCCAGCACCATCAGAGAAGAGTCATGAAGAAA  
 CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAA  
 GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTGGAAGC  
 CATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGAAGATTATGACCTTT  
 CAAAGATGAGAGACTTCATCAATAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA  
 GAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAATGGCAAAAGATCCAGGAGTCTTTCAA  
 CTGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATTCTGTGATTAAATTTTTTGACCCAAGG  
 GTTATTAGAAAAGTGTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCC  
 GTAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAA

## **FIGURE 150**

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG  
 QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK  
 FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE  
 VLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDETVSNTLTLTNGLE  
 RRTKTYSEDNFEELQYFPNFIYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV  
 SYLENLDEMIALQTKNKLEKNATDNISKLFPAPEKSHEETDSTKEEAAMEKEYGSLKDSTKDD  
 NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLSKMRDFINKQADAYVEKGILDK  
 EEAEAIKRIYSSL

### **N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

### **Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
 220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
 341, 369-372, 382-385, 386-389, 387-390

### **N-myristoylation sites:**

amino acids 143-148, 239-244

**FIGURE 151**

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCTGTGGAGCTCAA  
 GATGGTCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTATCTGC  
 ATAATAACCAAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCAATAAGGTGAAGAGATCAGC  
 GTGGTCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCGTATCCTGGGTGTCCAGGGTGAAG  
 CCAGTGCCCTGTATGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG  
 AGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTACCTTCTACCGCGGGACATGGGGCTCACC  
 TCCAGCTTCGAGTCCGGCTGCCTACCCGGGCTGGTTCCCTGTGCACGGTGCCTGAAGCCGATCAGCC  
 TGTCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCATCACAGACTTCTACTTCC  
 AGCAGTGTGACTAGGGCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAAGGGT  
 GAGTGGAGGAGACCCATGGCGGACAATCACTCTCTCTGCTCTCAGGACCCCACTGACTTAG  
 TGGGCACCTGACCACTTTGTCTTCTGGTTCCAGTTTGGATAAATCTGAGATTGGAGCTCAGT  
 CCACGGTCTCCCCACTGGATGGTGTACTGCTGTGGAACCTTGTAACCAATGTGGGGTAA  
 CTGGGAATAACATGAAAAGATTTCTGTGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCCTGCT  
 TAATGGTAAGTGAAGTGTACCCCTGAGCCCCGAGGCCAACCCATCCCCAGTTGAGCCTTATA  
 GGGTCAGTAGCTCTCCACATGAAGTCTGTCACTCACCCTGTGCAGGAGAGGGAGGTGGTCATA  
 GAGTCAGGGATCTATGGCCCTTGGCCAGCCCCACCCCTTCCCTTTAATCCTGCCACTGTCATA  
 TGCTACCTTTCCTATCTCTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTGTGTCAGAA  
 GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAA  
 GATACAATCAAAATCCCAGATGCTGGTCTTATTCCCATGAAAAAGTGTGTCATGACATATTGAGA  
 AGACCTACTTACAAAGTGGCATATATTGCAATTTATTTAATTAAGATACCTATTTATATATT  
 TCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTCAGGGTGGTGGCAGTAT  
 AGGTGATTTTCTTTTAAATTTCTGTTAATTTATCTGTATTTCCTAATTTTCTACAATGAAGATGA  
 ATTCCTTGATAAAAAATAAGAAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGA  
 TTGTCCTCAGCCTCCACTTCCCCAGAGTAAATTCAAATGAATCGAGCTCTGCTGCTCTGGTTGG  
 TTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGT  
 GTGGCTGGAATCTCTGGGTAAGGAACCTAAAGAACAAAAATCATCTGTAATTCCTTCTAGAAAG  
 GATCACAGCCCCCTGGGATTCGAAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA  
 ATTGTGTCCCCCTCAAATTCACATCCTTCTTGGAAATCTCAGTCTGTGAGTTTATTTGGAGATAAG  
 GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTGATGCTGGATGAAGGTAGACCTAAATTCATAT  
 GACTGGTTTCTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA  
 AAGATGAAGGCAGAGATCGGAGTTTTCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC  
 ATCAGAAGCTTGGAAGAGGCAAAGAAGAATTCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG  
 CTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGAATAAATTTCCGGCTGTTTTAA  
 GCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAACTAATAACAGCTGCTAAAATGATCCCTGT  
 CTCCTCGTGTTTACATTCGTGTGTGTCCCTCCCACAATGTACCAAGTTGTCTTTGTGACCAA  
 TAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTC  
 TACTTGAGCCCTCTCTCTGCCCACCCACGCCCCCAATCTATCTTGGCTCACTCGCTCTGGGGG  
 AAGCTAGCTGCCATGCTATGAGCAGGCCATAAAGAGACTTACGTGGTAAAAAATGAAGTCTCCT  
 GCCCACAGCCACATTAGTGAACTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT  
 AAGTTGCTCAGTTTGGTCTAAGTTGTTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG

## **FIGURE 152**

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESISVVPNRWLDASLSPVILGVQGGG  
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP  
VRLTQLPENGGWNAPITDFYFQQCD

### **N-myristoylation sites.**

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

### **Interleukin-1 signature.**

amino acids 111-131

### **Interleukin-1 proteins.**

amino acids 8-29, 83-120, 95-134, 64-103

# **FIGURE 153**

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC  
 CCTGCAGAAATCTGTGAGCTCTTTCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTCTCTTGG  
 CCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAAC  
 TTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA  
 CAACACAGACGTTTCGTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT  
 ATCTGATGAAGCAGGTGCTGAACTTCACCCTTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTTT  
 CAGCCTTATATGCAGGAGGTGGTGCCCTTCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA  
 TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAGC  
 TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAAGTGGATTTGCTGTTTATGTCTCTGAGAAAT  
 GCCTGCATTGACACAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTTCCCTGCTAGAAATAA  
 CAATTAGATGCCCCAAAGCGATTTTTTTTAAACAAAAGGAAGATGGGAAGCCAACTCCATCATG  
 ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTATTATA  
 AGACCAGAAGGTAGACTTCTAAGCATAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTTT  
 TATACACAGAAAACAATTTATTTTTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCCAT  
 TCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAA  
 TGTATTTATTATTATTATAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTAT  
 AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT  
 AGAGCTATAACATGTTTATTTGACCTCAATAAACACTTGGATATCCC

## **FIGURE 154**

MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL  
ADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLFPSDRFQPYMQEVVPFLARLSNRLS  
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDILFMSLRNACI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 54-58, 68-72, 97-101

**N-myristoylation sites.**

amino acids 14-20, 82-88

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 10-21

**FIGURE 155**

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT  
 CAGTCAGTGCCCGACTTGTGACTGAGTGTGCAGTGCCCGAGCATGTACCAGGTCACTGCAGAGGGC  
 TGCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC  
 TGCCAGGTTTGGGGCTGGGGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCAGAT  
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTTTCCTACAGGTGGTTGCAT  
 TCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGG  
 CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCCTAGAGCCTGCTAG  
 GCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCT  
 CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCAGGACCTGTACCACGCCCCGT  
 TGCCTGTGCCCCGCACTGCGTCAGCCTACAGACAGGCTCCCACATGGACCCCCGGGGCAACTCGGA  
 GCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACCCACA  
 AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTTCCTTAGCTTGTGTGTGTGTGCGGCCCCGT  
 GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTGGGAAACCTGGAGCCAGGTGTACA  
 ACCACTTGCCATGAAGGGCCAGGATGCCAGATGCTTGCCCCCTGTGAAGTGCTGTCTGGAGCAG  
 CAGGATCCCGGGACAGGATGGGGGGCTTTGGGGAAACCTGCACCTTCTGCACATTTTGAAAAGAG  
 CAGCTGCTGCTTAGGGCCGCCGGAAGCTGGTGTCTCTCATTTTCTCTCAGGAAAGGTTTTCAAA  
 GTTCTGCCCATTTCTGGAGGCCACCACTCCTGTCTCTTCTCTTTTCCCATCCCCTGCTACCCGT  
 GCCCAGCACAGGCACTTTCTAGATATTTCCCCCTTGCTGGAGAAGAAAGAGCCCCCTGGTTTTATT  
 TGTTTGTCTTACTCATCACTCAGTGAGCATCTACTTTGGGTGCATTCTAGTGTAGTTACTAGTCTT  
 TTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATAGAGATTTATCCAAATAAATAT  
 CTTTATTTAAAAATGAAAAA

## **FIGURE 156**

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHTYSHWPSCCPKQDTSEELLRWSTVPVPPLEPA  
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS  
ELLYHNQTVFYRRPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-32

**N-glycosylation site.**

amino acids 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 127-135

**N-myristoylation sites.**

amino acids 44-50, 150-156



**FIGURE 157**

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCGGTACCCCGAGAGCC  
GACCGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC  
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACAGTGTGCAACAGGGGACTATTCA  
ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGAAGGCCACCAA  
GATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTACAGCTGTGTGAGGTGCAATTACACAGAGG  
CCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCCTACATCGGCTTCCCTGTA  
GAGCTGAACACAGTCTATTTTCATTGGGGCCCATAATATTCCTAATGCAAATATGAATGAAGATGG  
CCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAA  
AGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAACATCACTGCTTGTAAGAAGAATGAGGAGACA  
GTAGAAGTGAAC TTCACAACCAC TCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCAC  
TATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA  
TTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGC  
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCT  
GGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCCTCTCCTCCTGCTGTCTCTGCTGGTGGCA  
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT  
TCTACCACCACACTACTGCCCCCATTAAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCA  
TCACACAATTTGTTACTTCACTGAATTTCTTCAAAACCATTGCAGAAGTGAGGTCACTCCTTGAAA  
AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCA  
GCAGACAAAGTCGTCTTCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA  
GAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCCTTTAACCTTTTCTGCA  
GTGATCTAAGAAGCCAGATTCACTCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA  
AAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT  
CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAGCCTGCCACG  
ATGGCTGCTGCTCCTTGTAG



# **FIGURE 159**

AGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT  
 GTCGATATTGGGGCTTGCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA  
 CTTTTTCCAAAAGCCTGAGAGTTGCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC  
 ATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG  
 GAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAGTGTAGGA  
 ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAA  
 GAGACCCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCT  
 GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTTAAGAGGTGCATATCC  
 ACTCAGCTGAAGAAG

## **FIGURE 160**

MTVKTLHGPPAMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPEŠCPPVPGGSMKLDIGIINEN  
QRVMSRNIESRSTSPWNYTVTWDPNRYPSSEVVQAQCRNLGCINAQKEDISMNSVPIQQETLVV  
RRKHQGCSSVSFQLEKVLVTVGCTCVTPVHHVQ

**Signal sequence:**

amino acids 1-30

**N-glycosylation site.**

amino acids 83-87

**N-myristoylation sites.**

amino acids 106-111, 136-141

## FIGURE 161

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAGG  
ACAGAGAGTGCACAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGGATTC  
CAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCCCTTGGGGGGGGCAGCAC  
AGGGCCTCAGGCCCTGGGTGCCACCTGGCACCTAGAAGATGCCCTGTGCCCTGGTCTTGCTGTCTT  
TGGCACTGGGCGCAAGCCCAAGTGGTCTTTCTCTGGAGAGGCTTGTGGGGCCTCAGGACGCTACC  
CACTGCTCTCCGGGCTCTCTGCCGCTCTGGGACAGTGACATACTCTGCCCTGCCCTGGGGACAT  
CGTGCCTGCTCCGGGCCCCGTGCTGGCGCCTACGCACCTGCAGACAGAGCTGGTGTGAGGTGCC  
AGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGCCGTGCATGGGCACTGG  
GAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAGGAA  
TGCTCTCTCCAGGCCCAAGTCGTGCTCTCTCTCCAGGCCCTACCTACTGCCCGCTGCGTCTGCTG  
TGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTCTGTGGGCTCTGTGGTATATGAC  
TGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCTATACTCAGCCCAGGTACGAGAA  
GGAACCTCAACACACACAGCAGCTGCCCTGCCCTGCCCTGGCTCAACGTGTGAGCAGATGGTGACA  
ACGTGCACTCTGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGGCTCTCCCTGTACTGGAATCAG  
GTCCAGGGCCCCCAAAACCCCGGTGGCACAAAACCTGACTGGACCGCAGATCATTACCTTGAA  
CCACACAGACCTGGTTCCTGCTCTGTATTGAGGTGTGGCCTCTGGAACCTGACTCCGTTAGGA  
CGAATCTGCCCCCTTACAGGGAGGACCCCGCGCACACCAGAACCTCTGGCAAGCCGCCGACTG  
CGACTGCTGACCCTGCAGAGCTGGCTGTGGACGCACCGTGTCTGCTGCCCGCAGAAGCGGCACT  
GTGCTGGCGGGCTCCGGGTGGGGACCCCTGCCAGCCACTGGTCCCACCGCTTTCTTGGGAGAACG  
TCACTGTGGACAAGGTTCTCGAGTTCCCATTTGCTGAAAGGCCACCCCTAACCTCTGTGTTTCAAGTG  
AACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGTCTGTGGGCTGACTCCCTGGGGCTCTCAAAGA  
CGATGTGCTACTGTTGGAGACACGAGGCCCCAGGACAACAGATCCCTCTGTGCCTTGGAAACCCA  
GTGGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTA  
CAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTG  
CCCCATGGACAAATACATCCACAAGCGCTGGGGCCCTCGTGTGGCTGGCCTGCCCTACTCTTTGCCG  
CTGGCCTTTCCCTCATCTCCTTCTCAAAAAGGATCACGCGAAAGGTGGCTGAGGCTCTTGAAA  
CAGGACGTCCGCTCGGGGGCGGGCCGCGAGGGGCGCGCGGCTCTGCTCCTTACTCAGCCGATGA  
CTCGGGTTTCGAGCGCTGGTGGGCGCCCTGGCGTCCGCCCTGTGCCAGCTGCCGCTGCGCGTGG  
CCGTAGACCTGTGGAGCCGTTCGTGAACCTGAGCGCGCAGGGGCCCCGTGGCTTGGTTTACGCGCAG  
CGGCGCCAGACCTGCAGGAGGGCGGGCGTGGTGGTCTTGTCTTCTCTCCCGGTGCGGTGGCGCT  
GTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCGGGGCGCACGGCCCGCACGACGCTTCC  
GCGCCTCGCTCAGCTGCGTGTCTGCCGACTTCTTGCAGGGCCGGGCGCCCGGCAGCTACGTGGGG  
GCCTGCTTCGACAGGCTGCTCCACCCGACGCGCTACCCGCCCTTTTCCGACCGTGGCCGCTCTT  
CACACTGCCCTCCCAACTGCCAGACTTCTTGGGGGCCCCTGAGCAGCCTCGCGCCCCGCGTTCGG  
GGCGGCTCCAAGAGAGCGGAGCAAGTGTCCCGGGCCCTTACCCAGCCCTGGATAGCTACTTC  
CATCCCCCGGGGACTCCCGCGCCGGGACCGGGGTGGGACCAGGGGCGGGACCTGGGGCGGGGGA  
CGGGACTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

**FIGURE 162**

MPVPWFLLSLALGRSPVVLSELRVLVGPQDATHCSPGLSCRLWDSILCLPGDIVPAPGPVLAPTHLQTELV  
 LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSFQAYPTARCVLLEV  
 QVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTPRYEKELNHTQQLPALPWLNVSAAGDNVHLVLNV  
 EEQHFGLSLYWNQVQGPPKPRWHKNLTGPIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQN  
 LWQAARLRLTLQSWLLDAPCSLPAAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ  
 VNSSEKLQEQECLWADSLGPKDDVLLLETRGPQDNRLCALEPSGCTSLPSKASTRAARLGEYLLQDLQS  
 GQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLKKDHAKGWLRLKQDVRSGAAARG  
 RAALLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAVFWHAQRRQTLQEGGVVLLFSP  
 GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFT  
 LPSQLPDLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

**Signal sequence:**

amino acids 1-20

**Transmembrane domain.**

amino acids 453-475

**N-glycosylation sites.**

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,  
 334-337, 357-360, 391-394

**Glycosaminoglycan attachment site.**

amino acids 583-586

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 552-555

**N-myristoylation sites.**

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,  
 692-697, 696-701, 700-705

**FIGURE 163**

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGCTGACCATCTTGACTGTGGGATCCCTGGCT  
GCTCACGCCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCCAGTCCAGCAACTTTGA  
AAACATCCTGACGTGGGACAGCGGGCCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA  
AGACGTACGGAGAGAGGGGACTGGGTGGCAAAGAAGGGCTGTGACGGGATCACCCGGAAGTCCTGC  
AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT  
GTCAGTGCGGGAGGCCGCTCAGCCACCAAGATGACTGACAGGTTGAGCTCTCTGCAGCACACTAC  
CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTGAGATGATTGTTTCATCCTA  
CCCCACGCCAATCCGTGCAGGCGATGGCCACCGGCTAACCTGGAAGACATCTTCCATGACCTG  
TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAGCAGAGAGA  
ATATGAGTTCTTCGGCCTGACCCCTGACACAGAGTTCCCTGGCACCATCATGATTTGCGTTCCCA  
CCTGGGCAAGGAGAGTGCCCCCTACATGTGCCGAGTGAAGACACTGCCAGACCGGACATGGACC  
TACTCCTTCTCCGGAGCCTTCCCTGTCTCCATGGGCTTCCCTCGTCGCAGTACTCTGCTACCTGAG  
CTACAGATATGTACCAAGCCGCTGCACCTCCCAACTCCCTGAACGTCCAGCGAGTCTGACTT  
TCCAGCCGCTGCGCTTCTATCCAGGAGCAGTCCCTGATCCCTGTCTTTGACCTCAGCGGCCCCAGC  
AGTCTGGCCCCAGCCTGTCCAGTACTCCAGATCAGGGTGTCTGGACCCAGGGAGCCCGCAGGAGC  
TCCACAGCGGCATAGCCTGTCCGAGATCACCTACTTAGGGCAGCCAGACATCTCCATCCTCCAGC  
CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCCACTGTCTATGCCCCAAACGCTGCCCTGAG  
GTCGGGCCCCCATCTATGCACCTCAGGTGACCCCGAAGCTCAATTCCCATTTACGCCCCACA  
GGCCATCTCTAAGGTCCAGCCTTCCCTCTATGCCCCCTCAAGCCACTCCGGACAGCTGGCCTCCCT  
CCTATGGGGTATGCATGGAAGGTTCTGGCAAAGACTCCCCACTGGGACACTTTCTAGTCCTAA  
CACCTTAGGCCTAAAGGTGAGCTTCAGAAAGAGCCACCAGCTGGAAGCTGCATGTTAGGTGGCCT  
TTCTCTGCAGGAGGTGACCTCCTTGGCTATGGAGGAATCCCAAGAAGCAAAATCATGACACAGC  
CCCTGGGGATTTGCACAGACAGAACATCTGACCCAAATGTGCTACACAGTGGGGAGGAAGGACA  
CCACAGTACCTAAAGGGCCAGCTCCCCCTCCTCTCCTCAGTCCAGATCGAGGGCCACCCCATGTC  
CCTCCCTTTGCAACCTCCTTCCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC  
TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCAGCCCTGAGACCTCAGACCTG  
GAGCAGCCACAGAAGTGGATTCTCTTTTCAGAGGCCCTGGCCCTGACTGTGCACTGGGAGTCCCTG  
AGGGGAATGGGAAAGGCTTGGTGCTTCCCTGCTCCCTACCCAGTGTACATCCTTGGCTGTCA  
ATCCCATGCCTGCCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGC  
AGAGGGAGTGGCATGCAGGGCCCCCTGCCATGGGTGCGCTCCTCACCAGGAACAAAGCAGCATGATA  
AGGACTGCAGCGGGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGCGTGCTCGCTGAGCCCTG  
CAAGGCAGAAATGACAGTGCAGGAGGAAATGCAGGGAACTCCCGAGGTCCAGAGCCCCACCTC  
CTAACACCATGGATTCAAAGTGCTCAGGGAATTTGCCCTCTCCTTGCCCCATTCTGGCCAGTTTC  
ACAATCTAGCTCGACAGAGCATGAGGCCCTGCCTCTTCTGTCAATTGTTCAAAGGTGGGAAGAGA  
GCCTGGAAAAGAACAGGCCCTGGAAAAGAACAGAGGAGGCTGGGCAGAACAGAACACCTGC  
ACTTCTGCCAAGGCCAGGGCCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCCTGCAGCTCA  
TTCCCAGCCAGGGCAACTGCCTGACGTTGCACGATTTGAGCTTATCTCTGATAGAACAAGC  
GAAATGCAGGTCCACCAGGGAGGGAGACACACAAGCCTTTCTGACGGCAGGAGTTTACAGCCCT  
ATCCTGAGAATGGGGTTTGAAGGAAGGTGAGGGCTGTGGCCCTGGACGGGTACAATAACACAC  
TGTACTGATGTACAACCTTTGCAAGCTCTGCCTTGGGTTGAGCCATCTGGGCTCAAATTCAGC  
CTCACCCTCACAAGCTGTGTGACTTCAAACAATGAAATCAGTGCCAGAACCTCGGTTTCCCTC  
ATCTGTAATGTGGGGATCATAACACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG  
TCTTTAAAGTGCTTAATAGTGCTTGGTACATGGGCAGTGCCCAATAAACGGTAGCTATTTAAAAA  
AAAAAAA





## FIGURE 165

TGGCCTACTGGAaaaaaaaaaaaaaaaaaaaaaAGTCACCCGGGCCCGCGGTGGCCACAACATGG  
CTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGGCCAG  
TCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTGCAGCAT  
GTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGTGAATTTTA  
AAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAAC TTTGGGCTGGA  
AGTGTGTAACACAGTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCATAAATACACGGA  
AGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGGAGGAAGAGATGATT  
TTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGACTCTGTACCTGAAGAG  
TCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGA  
ACTTGACCCTGTGCCTGAGCCCCGAGGCATTTCAGAGCTGATTTCAGAGGATGGAGAAGGTGCTTTCT  
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCTCACACCAGCGGT  
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATTCTGCACGATAA  
ATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA  
AGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGC GTTATT  
CATTACAGCAAAGGATTTTCGTTGGCATCAAAATCTAAGTTTGT TTTTACAAAGATTGTTTTTAGTA  
CTAAGCTGCCTTGGCAGTTTGCATTTTGGAGCCAAACAAAAATATATTATTTTCCCTTCTAAGTA  
AAAAAAAAAAAAAAAAAAAAA



## FIGURE 167

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCTCAGAGGCCGGGGAAGAGAAGCAAAGCGC  
AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCCTCTAGGACATACACGGGACCCCTAACTTC  
AGTCCCCCAAACGCGCACCTCGAAGTCTTGAACCTCAGCCCCGCACATCCACGCGCGGCACAGG  
CGCGGCAGGCGGCAGGTCCCCGGCCGAAGGCGATGCGCGCAGGGGGTGGGCGAGCTGGGCTCGGGC  
GGCGGGAGTAGGGCCCGCAGGAGGAGGAGGAGGCTGCATATTCAGAGTCGCGGGCTGCGCCCTG  
GGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGATGAGCCGCGTGG  
TCTCGCTGCTGCTGGGCGCCGCGCTGCTGCTGCGGCCACGGAGCCTTCTGCCGCCGCGTGGTCAAGC  
GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCCTACTTCCATGAAC  
GTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTTGTGAGAGTGAGGAGGAGTCCCTCCTCA  
GCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG  
ACAGGGATTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGAATGGAGATGGGCAACATCTGG  
TGCCTGCCCAGATCTCTACCAAGTGGTCTGATGGAAGCAATCCCAGTACCGAACTGGTACACAG  
ATGAACCTTCTGCGGAAGTGAAAAGTGTGTTGTGATGATCACCACCAACTGCCAATCCTGGC  
CTTGGGGGTCCCTACCTTTACCAAGTGGATGATGACAGGTGTAACATGAAGCACAATTATATTTG  
CAAGTATGAACCAGAGATTAATCCAACAGCCCCGTGAGAAAAGCCTTATCTTACAAATCAACCAG  
GAGACACCCATCAGAATGTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTT  
ATACCAACAATACCCCTGCTCTTACTGATGACTGGTGTCTTTTGAACCTGTTGTTTCCAGATGCT  
GCATAAAAGTAAAGGAAGAACAACAACTAGTCCAAACAGTCTACACTGTGGATTTCAAAGAGTA  
CCAGAAAAGAAAGTGGCATGGAAGTATAATAACTCATGACTTGGTTCAGAAATTTTGTAAATCT  
GGATCTGTATAAGGAATGGCATCAGAACAATAGCTTGGAAATGGCTTGAAATCACAAGGATCTGC  
AAGATGAACGTGAAGCTCCCCCTTGAGGCAATATTAAGTAATTTTATATGTCTATTATTTCA  
TTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAA  
ACTTCAAACCTTCAAGCAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTA  
TGTGTGTTAGAAGCAATTCCTTTTATTTCTTTCACCTTTCATAAGTTGTTATCTAGTCAATGTAA  
TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGTTGATAAAA  
ATGAACCTGTTCTAATATTTATTTTATGGCATCTCATTTTCAATACATGCTCTTTTGATTAAAG  
AACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGT  
TTTCTCGAAATAATTCATCTTTACAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTCAGA  
AATAAGAAGCTATTTTCAATTAAGTGTGATATAAACCTCCTCAACATTTTACTTAGAGGCAAGGAT  
TGTCTAATTTCAATTTGTGCAAGACATGTGCCTTATAATTATTTTACTTAAATTAACAGATT  
TTGTAATAATGTAACCTTTGTTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAG  
TGACATACACAATATAAATCATATGTCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTCTGA  
GGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTGTTCGGGGTTTGGG  
ATTGACACTGGAGGCAGATAGTTGCAAGTGTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTG  
ACTATATTAGTATACAAAGAGGTGATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG  
ACAAGCACAGCACAGACATTTTAGGAAGGAAAGGAACACGAAATCGTGTGAAAATGGGTTGG  
AACCATCAGTGATCGCATATTCATTGATGAGGGTTTGGCTTGAGATAGAAAATGGTGGCTCCTTT  
CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTCTTCTCAAGAGAAAGTTGTAACCT  
CTGGTCTTCATATGTCCCTGTGCTCCTTTAACCATAAAGAGTTCTTGTCTGGGGGAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 168**

MSRVVSLLLGAALLCGHGAF  
CRRVVSQKVCFADFKHPCYK  
MAYFHELSSRVSFQEARLACESE  
GGVLLSLENEAEQKLI  
ESMLQNLTKPGTGISDGD  
FWIGLWRNGDGTSGACPD  
LYQWSDGSNSQYRNWYT  
DEPSCGSEKCVVMYHQPT  
ANPGLGGPYLYQWDDRC  
NMKHNYICKYEPEINPT  
APVEKPYLTNQPGDTHQ  
NVVVTEAGIIPNLIYVVI  
PTIPLLLLILVAFGTCCF  
QMLHKS  
KGRTKTSPNQSTLWISK  
STRKESGMEV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domain:**

amino acids 214-235

#### **N-glycosylation sites.**

amino acids 86-89, 255-258

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

#### **N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145, 212-217